

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<212> DNA  
<213> Homo sapiens

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Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
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Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
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Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
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305          310          315          320
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325          330          335
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340          345          350
Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
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370          375          380
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Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
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Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
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Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
450          455          460
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465          470          475          480
Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser
485          490          495
Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
500          505          510
Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
515          520          525
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530          535          540
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660 665 670
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675 680 685
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln
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Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
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740 745 750
Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
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Asp Thr Asp Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro
      1205      1210      1215
Gly Ala Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys
      1220      1225      1230
Pro Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp
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Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys Glu Asn Asn
      1285      1290      1295
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Thr Pro Leu Ser Tyr Thr His Trp Arg Ala Gly Arg Pro Thr Ile Lys
      1330      1335      1340
Asn Glu Lys Phe Leu Ala Gly Leu Ser Thr Asp Gly Phe Trp Asp Ile
      1345      1350      1355
Gln Thr Phe Lys Val Ile Glu Glu Ala Val Tyr Phe His Gln His Ser
      1365      1370      1375
Ile Leu Ala Cys Lys Ile Glu Met Val Asp Tyr Lys Glu Glu His Asn
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Ser Gly Gly His Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe
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Leu Glu Asp Ile Val Lys Arg Asp Gly Phe Pro Leu Trp Val Gly Leu
      1445      1450      1455
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      1475      1480      1485
Val Leu Asp Pro Lys Gly Thr Trp Lys His Glu Lys Cys Asn Ser
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      1505      1510      1515
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<210> 148  
<211> 499  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mouse-Human hybrid fusion protein

<400> 148  
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20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser

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Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105						110		
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Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145					150					155					160
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
			180					185					190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195				200						205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210				215						220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225					230					235					240
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp
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Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
	370				375						380				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
					390					395					400
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
			405						410					415	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
			420					425					430		
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
			435				440					445			
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
	450					455					460				
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
					470					475					480
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
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Pro	Gly	Lys													

<210> 149  
<211> 1470  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse-Human hybrid fusion protein

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ccttgcgggc aacaatccat tcacttggga ggagtatttg aattgcaacc aggtgcttcg 1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt 1440
ggcttactca aactcgagtg ataactctaga                                     1470
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<210> 150

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse-Human hybrid fusion protein

<400> 150

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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
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	290					295					300				
Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	Leu
305					310					315					320
Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly
				325					330					335	
Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser
			340					345					350		
Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met
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Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys
	370					375					380				
Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn
385					390					395					400
Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys
				405					410					415	
Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His
			420					425					430		
Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	Val
		435					440					445			
Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	Pro
	450					455					460				
Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	Lys
465					470					475					480
Leu	Glu														

<210> 151  
<211> 1290  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mouse-Human hybrid fusion protein

<400> 151

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taccagcaga	agccaggatc	ctccccaaa	ccctggattt	atgccccatc	caactggct	240
tctggagtcc	ctgctcgctt	cagtggcagt	gggtctggga	ctcttactc	tctcacaatc	300
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<210> 152  
<211> 422  
<212> PRT  
<213> Artificial Sequence

<220>

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<223> Mouse-Human hybrid fusion protein

<400> 152

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 20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
260      265      270
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
275      280      285
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
290      295      300
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
305      310      315      320
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
325      330      335
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
340      345      350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Arg Ala
355      360      365
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
370      375      380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
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Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
405      410      415
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420

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<210> 153

<211> 3630

<212> DNA

<213> Homo sapiens

<400> 153

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cgcgcggtg agaaccgccg ggaccgcacg tgggcgccgc gcgcttcccc cgcttcccag 180
gtgggcgccg gccgccaggc cacctcacgt ccggcccccg ggatgcgcgt cctcctcgcc 240

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<400> 162

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<211> 822  
<212> DNA  
<213> Homo sapiens

<400> 163

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 Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala  
 35 40 45  
 Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe  
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 65 70 75 80  
 Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro  
 85 90 95  
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<210> 165  
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 <213> Homo sapiens

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35 40 45  
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85 90 95  
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115 120 125  
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Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn  
165 170 175  
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<210> 167  
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<212> DNA  
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3

<210> 168  
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<213> Homo sapiens - to be filled in

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<400> 168  
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<211> 3084  
<212> DNA  
<213> Homo sapiens

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<210> 170  
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<212> PRT  
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Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala  
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Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
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<212> DNA  
<213> Homo sapiens

<400> 171

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 <212> PRT  
 <213> Homo sapiens

<400> 172

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<211> 1060

<212> DNA

<213> Homo sapiens

<400> 173

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<210> 174

<211> 235

<212> PRT

<213> Homo sapiens

<400> 174

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35     40     45
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50     55     60
Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65     70     75     80
Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
85     90     95
Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
100    105    110
Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
115    120    125
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
130    135    140
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145    150    155    160
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
165    170    175
Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
180    185    190
Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
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<210> 175

<211> 4740

<212> DNA

<213> Homo sapiens

<400> 175

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 <213> Homo sapiens

<400> 176  
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 Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val  
 35 40 45  
 Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr  
 50 55 60  
 Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val  
 65 70 75 80  
 Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr  
 85 90 95  
 Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr  
 100 105 110  
 Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser  
 115 120 125  
 Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys  
 130 135 140  
 Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser  
 145 150 155 160  
 Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val  
 165 170 175  
 Met Glu Gln Leu Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr  
 180 185 190  
 Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn  
 195 200 205  
 Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Gly Arg  
 210 215 220  
 Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn  
 225 230 235 240  
 Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile  
 245 250 255  
 Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile  
 260 265 270  
 Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly  
 275 280 285  
 Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala  
 290 295 300  
 Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala  
 305 310 315 320  
 Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu  
 325 330 335  
 Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln  
 340 345 350  
 Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr  
 355 360 365  
 Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys  
 370 375 380  
 Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn  
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 Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val  
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 Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val  
 450 455 460  
 Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro  
 465 470 475 480  
 His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu  
 485 490 495  
 Pro Arg Gly Gln Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly  
 500 505 510  
 Glu Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu  
 515 520 525  
 Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro  
 530 535 540  
 Gly Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser  
 545 550 555 560  
 Gly Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Lys  
 565 570 575  
 Leu Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln  
 580 585 590  
 Asp Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly  
 595 600 605  
 His Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile  
 610 615 620  
 Met Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn  
 625 630 635 640  
 Asp Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu  
 645 650 655  
 His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln  
 660 665 670  
 Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser  
 675 680 685  
 Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln  
 690 695 700  
 Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro  
 705 710 715 720  
 Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe  
 725 730 735  
 Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val  
 740 745 750  
 Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu  
 755 760 765  
 Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr  
 770 775 780  
 Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu  
 785 790 795 800  
 Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg  
 805 810 815  
 Thr Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val  
 820 825 830  
 Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys  
 835 840 845  
 Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser  
 850 855 860  
 Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe  
 865 870 875 880  
 Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu  
 885 890 895  
 Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn  
 900 905 910  
 Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met  
 915 920 925  
 Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala  
 930 935 940  
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 Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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Ser	Asp	Phe	Leu	Ala	Glu	Leu	Arg	Lys	Ala	Pro	Val	Val	Asn	Cys	Ser
Ile	Ala	Val	Cys	Gln	Arg	Ile	Gln	Cys	Asp	Ile	Pro	Phe	Phe	Gly	Ile
Gln	Glu	Glu	Phe	Asn	Ala	Thr	Leu	Lys	Gly	Asn	Leu	Ser	Phe	Asp	Trp
Tyr	Ile	Lys	Thr	Ser	His	Asn	His	Leu	Leu	Ile	Val	Ser	Thr	Ala	Glu
Ile	Leu	Phe	Asn	Asp	Ser	Val	Phe	Thr	Leu	Leu	Pro	Gly	Gln	Gly	Ala
Phe	Val	Arg	Ser	Gln	Thr	Glu	Thr	Lys	Val	Glu	Pro	Phe	Glu	Val	Pro
Asn	Pro	Leu	Pro	Leu	Ile	Val	Gly	Ser	Ser	Val	Gly	Gly	Leu	Leu	Leu
Leu	Ala	Leu	Ile	Thr	Ala	Ala	Leu	Tyr	Lys	Leu	Gly	Phe	Phe	Lys	Arg
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<211> 1364

<212> DNA

<213> Homo sapiens

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<210> 178

<211> 375

<212> PRT

<213> Homo sapiens

<400> 178

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Val	Ser	Ala	Thr	Thr	Pro	Glu	Pro	Cys	Glu	Leu	Asp	Asp	Glu	Asp
				20				25				30		Phe
Arg	Cys	Val	Cys	Asn	Phe	Ser	Glu	Pro	Gln	Pro	Asp	Trp	Ser	Glu
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85 90 95  
Gly Ala Ala Gln Val Pro Ala Gln Leu Val Gly Ala Leu Arg Val  
100 105 110  
Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile  
115 120 125  
Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu  
130 135 140  
Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp  
145 150 155 160  
Leu Ala Glu Leu Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser  
165 170 175  
Ile Ala Gln Ala His Ser Pro Ala Phe Ser Cys Glu Gln Val Arg Ala  
180 185 190  
Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly  
195 200 205  
Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile  
210 215 220  
Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val  
225 230 235 240  
Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu  
245 250 255  
Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys  
260 265 270  
Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu  
275 280 285  
Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu  
290 295 300  
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305 310 315 320  
Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr  
325 330 335  
Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys  
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<210> 179

<211> 2633

<212> DNA

<213> Homo sapiens

<400> 179

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agccgaagtc	aagacgg tcc	ccaatgacgc	cacacagaca	aaggagaacg	agagcaaagc	2580
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<212> PRT  
<213> Homo sapiens

<400> 180

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Val	Gly	Glu	Ser	Lys	Phe	Phe	Leu	Cys	Gln	Val	Ala	Gly	Asp	Ala	Lys
		35					40					45			
Asp	Lys	Asp	Ile	Ser	Trp	Phe	Ser	Pro	Asn	Gly	Glu	Lys	Leu	Thr	Pro
	50					55					60				
Asn	Gln	Gln	Arg	Ile	Ser	Val	Val	Trp	Asn	Asp	Asp	Ser	Ser	Ser	Thr
65				70					75					80	
Leu	Thr	Ile	Tyr	Asn	Ala	Asn	Ile	Asp	Asp	Ala	Gly	Ile	Tyr	Lys	Cys
			85					90					95		
Val	Val	Thr	Gly	Glu	Asp	Gly	Ser	Glu	Ser	Glu	Ala	Thr	Val	Asn	Val
		100					105					110			
Lys	Ile	Phe	Gln	Lys	Leu	Met	Phe	Lys	Asn	Ala	Pro	Thr	Pro	Gln	Glu
		115					120				125				
Phe	Arg	Glu	Gly	Glu	Asp	Ala	Val	Ile	Val	Cys	Asp	Val	Val	Ser	Ser
	130					135					140				
Leu	Pro	Pro	Thr	Ile	Ile	Trp	Lys	His	Lys	Gly	Arg	Asp	Val	Ile	Leu
145				150					155					160	
Lys	Lys	Asp	Val	Arg	Phe	Ile	Val	Leu	Ser	Asn	Asn	Tyr	Leu	Gln	Ile
				165				170					175		
Arg	Gly	Ile	Lys	Lys	Thr	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Glu	Gly	Arg
		180					185						190		
Ile	Leu	Ala	Arg	Gly	Glu	Ile	Asn	Phe	Lys	Asp	Ile	Gln	Val	Ile	Val
		195					200					205			
Asn	Val	Pro	Pro	Thr	Ile	Arg	Ala	Arg	Gln	Asn	Ile	Val	Asn	Ala	Thr
210						215					220				
Ala	Asn	Leu	Gly	Gln	Ser	Val	Thr	Leu	Val	Cys	Asp	Ala	Glu	Arg	Phe
225					230					235				240	
Pro	Glu	Pro	Thr	Met	Ser	Trp	Thr	Lys	Asp	Gly	Glu	Gln	Ile	Glu	Gln
				245					250					255	
Glu	Glu	Asp	Asp	Glu	Lys	Tyr	Ile	Phe	Ser	Asp	Asp	Ser	Ser	Gln	Leu
		260						265					270		
Thr	Ile	Lys	Lys	Val	Asp	Lys	Asn	Asp	Glu	Ala	Glu	Tyr	Ile	Cys	Ile
		275					280					285			
Ala	Glu	Asn	Lys	Ala	Gly	Glu	Gln	Asp	Ala	Thr	Ile	His	Leu	Lys	Val

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290 295 300  
Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu  
305 310 315  
Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile  
325 330 335  
Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu  
340 345 350  
Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser  
355 360 365  
Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile  
370 375 380  
Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu  
385 390 395 400  
Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr  
405 410 415  
Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro  
420 425 430  
Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser  
435 440 445  
Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu  
450 455 460  
Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr  
465 470 475 480  
Ala Val Asn Arg Ile Gly Gln Glu Ser Phe Glu Phe Ile Leu Val Gln  
485 490 495  
Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser  
500 505 510  
Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val  
515 520 525  
Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val  
530 535 540  
Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile  
545 550 555 560  
Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu  
565 570 575  
Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu  
580 585 590  
Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu  
595 600 605  
Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys  
610 615 620  
Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg  
625 630 635 640  
Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser  
645 650 655  
Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val  
660 665 670  
Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe  
675 680 685  
Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser  
690 695 700  
Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val  
705 710 715 720  
Ile Phe Val Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu  
725 730 735  
Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys  
740 745 750  
Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala  
755 760 765  
Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu  
770 775 780  
Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn  
785 790 795 800  
Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys  
805 810 815  
Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys  
820 825 830  
Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala  
835 840 845



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<210> 181  
<211> 1702  
<212> DNA  
<213> Homo sapiens

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<400> 181
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tagggaatct tgagaataaa gatgagctct gaaaattggt tcgtagcaga gaacagctct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccattttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgctctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgtag gtagagagga acactgggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atggcaaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc catagagact 780
ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacagggtga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaaataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgtttgta ctagatactg aatgtaaaca aaggaattat ggctggtaac ataggttttt 1140
agtctaattg aatcccttaa actcaggagag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatattttctc tctttttaga gaaatttgcc aattttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtatttta tttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacataatt ctttgccttt ataactcttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagtgt tggaaaaatg 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg ttgtgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt ttttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaa aaaaaaaaaa aa 1702
```

<210> 182  
<211> 199  
<212> PRT  
<213> Homo sapiens

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<400> 182
Met Ser Ser Glu Asn Cys Phe Val Ala Glu Asn Ser Ser Leu His Pro
1 5 10 15
Glu Ser Gly Gln Glu Asn Asp Ala Thr Ser Pro His Phe Ser Thr Arg
20 25 30
His Glu Gly Ser Phe Gln Val Pro Val Leu Cys Ala Val Met Asn Val
35 40 45
Val Phe Ile Thr Ile Leu Ile Ile Ala Leu Ile Ala Leu Ser Val Gly
50 55 60
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
65 70 75 80
His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
85 90 95
Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
100 105 110
Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
115 120 125
Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
130 135 140
Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu
145 150 155 160
Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
165 170 175
Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
180 185 190
Ile Cys Asn Lys Pro Tyr Lys
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195

<210> 183  
<211> 1642  
<212> DNA  
<213> Homo sapiens

<400> 183  
ctctaaaggt tcggggggtgg aatccttggg ccgctgggca agcggcgaga cctggccagg 60  
gccagcgagc cgaggacaga gggcgcacgg agggccgggc cgcagccccg gccgcttgca 120  
gaccccgcca tggacccggt cctgggtgctg ctgcactcgg tgtcgtccag cctgtcagac 180  
agcgagctga ccgagctcaa gttcctatgc ctcgggcgcg tgggcaagcg caagctggag 240  
cgcgctgcaga ggggcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 300  
gggcacaccg agctcctgcg cgagctgctc gcctccctgc ggcggcacga cctgctgcgg 360  
cgcgctgcagc acttcgagggc gggggcgggc gcccggggcg cgcctgggga agaagacctg 420  
tgtgagcat ttaacgtcat atgtgataat gtggggaaag attggagaag gctggctcgt 480  
cagctcaaaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 540  
acagagcgtg tgcgggagtc actgagaatc tggagaaga cagagaagga gaacgcaaca 600  
gtggccacc tgggtggggc tctcaggtcc tgccagatga acctgggtgc tgacctgta 660  
caagaggttc agcaggcccc tgacctccag aacaggagtg gggccatgtc cccgatgtca 720  
tggaactcag acgcatctac ctccgaagcg tcctgatggg ccgctgcttt gcgctggtgg 780  
accacaggca tctacacagc ctggactttg gttctctcca ggaaggtagc ccagcactgt 840  
gaagaccag caggaagcca ggctgagtga gccacagacc acctgcttct gaactcaagc 900  
tgcgtttatt aatgcctctc ccgcaccagg ccgggcttgg gccctgcaca gatatttcca 960  
tttcttcctc actatgacac tgagcaagat ctgtctcca ctaaatgagc tcctgcggga 1020  
gtagttggaa agttggaacc gtgtccagca cagaaggaat ctgtgcagat gaggcagcac 1080  
actgttactc cacagcggag gagaccagct cagaggccca ggaatcggag cgaagcagag 1140  
aggtggagaa ctgggatttg aacccccgcc atcttcacc agagcccatg ctcaaccact 1200  
gtggcggtct gctgcccctg cagttggcag aaaggatgtt ttgtccatt tccttggagg 1260  
ccaccgggac agacctggac actagggtca cgtgggtgc ggcggggtgc tgggtgggg 1320  
ctgggggtgg ggtggggaga cctgggtggc cgtgggtccag ctcttggccc ctgtgtgagt 1380  
tgagttcct ctctgagact gctaagttag ggagtgatg gttgccagga cgaattgaga 1440  
taatatctgt gaggtgctga tgagtgattg acacacagca ctctctaaat cttccttgtg 1500  
aggattatgg gtccctgcaat tctacagttt cttactgttt tgtatcaaaa tcactatctt 1560  
tctgataaca gaattgccaa ggcagcgggg tctcgtatct ttaaaaagca gtcctcttat 1620  
tcctaaggtg atcctattaa aa 1642

<210> 184  
<211> 208  
<212> PRT  
<213> Homo sapiens

<400> 184  
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser  
1 5 10 15  
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly  
20 25 30  
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met  
35 40 45  
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg  
50 55 60  
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp  
65 70 75 80  
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp  
85 90 95  
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp  
100 105 110  
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser  
115 120 125  
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser  
130 135 140  
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His  
145 150 155 160  
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu  
165 170 175  
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala  
180 185 190  
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
195 200 205

<210> 185  
<211> 1475  
<212> DNA  
<213> Homo sapiens

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<400> 185
ggcaccgaggg agcggagcct ggcgggctg ggaacccagg ccccgccgag gcggccagga 60
ggtgagatgg cagctgggca aaatgggcac gaagagtggg tgggcagcgc atacctgttt 120
gtggagtcct cgctggacaa ggtggtcctg tcggatgcct acgcgcaccc ccagcagaag 180
gtggcagtgt acagggctct gcaggctgcc ttggcagaga gcggcgggag cccggacgtg 240
ctgcagatgc tgaagatcca ccgcagcgac ccgcagctga tcgtgcagct gcgattctgc 300
ggcgggcagc cctgtggccg cttcctccgc gcctaccgcg agggggcgct gcgcgccgcg 360
ctgcagagga gcctggcggc cgcgctcgcc cagcactcgg tgccgctgca actggagctg 420
cgcgccggcg ccgagcggct ggacgctttg ctggcggacg aggagcgctg tttgagttgc 480
atcctagccc agcagcccga ccggctccgg gatgaagaac tggctgagct ggaggatgctg 540
ctgcgaaatc tgaagtgcgg ctctggggcc cggggtggcg acggggaggt cgcttcggcc 600
cccttgacgc ccccggtgcc ctctctgtcg gaggatgaagc cgccgccgcc gccgccacct 660
gcccagactt ttctgttcca gggtcagcct gtagtgaatc ggccgctgag cctgaaggac 720
caacagacgt tcgcgcgctc tgtgggtctc aaatggcgca aggtggggcg ctactgcag 780
cgaggctgcc gggcgctgct ggacccggcg ctggactcgc tggcctacga gtacgagcgc 840
gagggactgt acgagcaggc cttccagctg ctgcggcgct tcgtgcaggc cgagggccgc 900
cgcgccacgc tgcagcgcct ggtggaggca ctgcaggaga acgagctcac cagcctggca 960
gaggacttgc tgggcctgac cgatcccaat ggcggcctgg cctagaccag ggtgagacc 1020
agcttttggg gaacctggat ggccttaggg ttcttctgct ggctattgct gaacctctgt 1080
ccatccacgg gacctgaaa ctccacttgg cctatctgct ggacctgctg gggcagagtt 1140
gattgccttc cccaggagcc agaccactgg ggggtgcatca ttggggattc tgcctcaggt 1200
actttgatag agtggtgggt gggggggacc tgctttggag atcagcctca ccttctccca 1260
tcccagaagc ggggcttaca gccagccctt acagtttcac tcatgaagca ccttgatctt 1320
tgggttcctg gacttcatcc tgggtgctgc agatactgca gtgaagtaaa acaggaatca 1380
atcttgccctg cccccagctc acactcagcg tgggaccccg aatgttaagc aatgataata 1440
aagtataaca cggaaaaaaa aaaaaaaaaa aaaaaa 1475
```

<210> 186  
<211> 312  
<212> PRT  
<213> Homo sapiens

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<400> 186
Met Ala Ala Gly Gln Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
1 5 10 15
Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
20 25 30
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
35 40 45
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
50 55 60
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
65 70 75 80
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
85 90 95
Ala Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val
100 105 110
Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
115 120 125
Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
130 135 140
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
145 150 155 160
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
165 170 175
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
180 185 190
Pro Pro Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
195 200 205
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
210 215 220
```

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly  
225 230 235 240  
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr  
245 250 255  
Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe  
260 265 270  
Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala  
275 280 285  
Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu  
290 295 300  
Thr Asp Pro Asn Gly Gly Leu Ala  
305 310

<210> 187  
<211> 600  
<212> DNA  
<213> Homo sapiens

<400> 187  
atggaagcca gagacaagca ggtactccgc tccctgcgtc tggagctggg tgccgaggtg 60  
ctggtggaag gactggttct tcagtacatt taccaggaag gaattttgac agaaaaccac 120  
attcaagaaa tcaaagctca aaccacaggc ctccggaaga caatgctgtt gctggacatc 180  
ctgccttcca ggggcccaca agcttttgac accttcctcg attccctcca ggaatttccc 240  
tgggtaagag agaagctgga gaaggcgaga gaggaagtca cagccgagct gcctacaggt 300  
gactggatgg ccggaatccc ctacacatc ctacagcagct cgccatcaga ccagcagatt 360  
aaccagctgg ctcaagaagt agggccggag tgggagcccg tggctcctgtc tctgggactg 420  
tcccagaccg acatctaccg ctgcaaggcc aaccatcccc acaacgtgca ttcgaggtg 480  
gtggaggcct ttgtccgctg gcgccagcgt ttgggaagc aggccacctt cctaagctta 540  
cacaagggcc tccaggcagt ggaggctgat ccctccctgc tccagcacat gctggagtga 600

<210> 188  
<211> 199  
<212> PRT  
<213> Homo sapiens

<400> 188  
Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu  
1 5 10 15  
Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln  
20 25 30  
Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Lys Ala Gln Thr  
35 40 45  
Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg  
50 55 60  
Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro  
65 70 75 80  
Trp Val Arg Glu Lys Leu Glu Lys Ala Arg Glu Glu Val Thr Ala Glu  
85 90 95  
Leu Pro Thr Gly Asp Trp Met Ala Gly Ile Pro Ser His Ile Leu Ser  
100 105 110  
Ser Ser Pro Ser Asp Gln Gln Ile Asn Gln Leu Ala Gln Lys Leu Gly  
115 120 125  
Pro Glu Trp Glu Pro Val Val Leu Ser Leu Gly Leu Ser Gln Thr Asp  
130 135 140  
Ile Tyr Arg Cys Lys Ala Asn His Pro His Asn Val His Ser Gln Val  
145 150 155 160  
Val Glu Ala Phe Val Arg Trp Arg Gln Arg Phe Gly Lys Gln Ala Thr  
165 170 175  
Phe Leu Ser Leu His Lys Gly Leu Gln Ala Val Glu Ala Asp Pro Ser  
180 185 190  
Leu Leu Gln His Met Leu Glu  
195

<210> 189  
<211> 1642  
<212> DNA

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<213> Homo sapiens

<400> 189  
ctctaaaggt tcgggggtgg aatccttggg ccgctgggca agcggcgaga cctggccagg 60  
gccagcgagc cgaggacaga gggcgacagg agggccgggc cgcagcccg gccgcttgca 120  
gaccccgcca tggacccgtt cctgggtgctg ctgcactcgg tgtcgtccag cctgtcgagc 180  
agcgagctga ccgagctcaa gttcctatgc ctccggcgcg tgggcaagcg caagctggag 240  
cgcggtgcaga gcggcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 300  
gggcacaccg agctcctgcg cgagctgctc gcctccctgc ggcgccacga cctgtgctgg 360  
cgcgctcgagc acttcgagggc gggggcgggc gccgggggccc gccttgggga agaagacctg 420  
tgtgcagcat ttaacgctcat atgtgataat gtgggggaaag attggagaag gctggctcgt 480  
cagctcaaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 540  
acagagcggtg tgcgggagtc actgagaatc tggaagaaca cagagaagga gaacgcaaca 600  
gtggcccacc tgggtgggggc tctcaggtcc tgccagatga acctgggtggc tgacctggta 660  
caagaggttc agcaggcccg tgacctccag aacaggagtg gggccatgtc cccgatgtca 720  
tggaactcag acgcatctac ctccgaagcg tcttgatggg ccgctgcttt gcgctgggtg 780  
accacaggca tctacacagc ctggactttg gttctctcca ggaaggtagc ccagcactgt 840  
gaagaccag caggaagcca ggctgagtga gccacagacc acctgcttct gaactcaagc 900  
tgcgtttatt aatgcctctc tgagcaagat cttgtctcca cttaaagagc tctgctggga 1020  
tttcttcttc actatgacac gtgtccagca cagaaggaat ctgtgcagat gagcagtcac 1080  
gtagttggaa agtttgaacc gagaccagct cagaggccca ggaatcgag cgaagcagag 1140  
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<212> PRT

<213> Homo sapiens

<400> 190

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<211> 3492

<212> DNA

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<400> 191

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<211> 425

<212> PRT

<213> Homo sapiens

<400> 192

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 50 55 60  
 Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg  
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 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu  
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 100 105 110  
 Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys  
 115 120 125  
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 130 135 140  
 Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met  
 145 150 155 160  
 Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly  
 165 170 175  
 Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln  
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 Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
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 Arg Gly Thr Gln Gly Pro Glu Gln His Leu Leu Ile Thr Ala Pro  
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 305 310 315 320  
 Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro  
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 Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr  
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Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln  
50 55 60  
Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
65 70 75 80  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser  
85 90 95  
Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe  
100 105 110  
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115 120 125  
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145 150 155 160  
Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile  
165 170 175  
Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala  
180 185 190  
Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp  
195 200 205  
Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly  
210 215 220  
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225 230 235 240  
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245 250 255  
Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn  
260 265 270  
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275 280 285  
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp  
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 355 360 365  
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 65 70 75 80  
 Lys Tyr Gly Asn His Cys Tyr Tyr Phe Ser Val Glu Glu Lys Asp Trp  
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 Asn Ser Ser Leu Glu Phe Cys Leu Ala Arg Asp Ser His Leu Leu Val  
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 115 120 125  
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 130 135 140  
 Asp Gly Ser Pro Leu Asn Phe Ser Arg Ile Ser Ser Asn Ser Phe Val  
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Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
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Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
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actatgaaag aggacgaaaa aagatacaat gaaagaattt cagggttagg gctgacacca 360  
gaacagaaac agaaaaaggc cgcgttatct gcttcagaag gagaggaggt tcctcaagac 420  
aaggcgccaa gtcattgttc tttcctgcta attggtggag gcacagctgc ttttgctgca 480  
gccagatcca tccgggctcg ggatcctggg gccagggtac tgattgtatc tgaagatcct 540  
gagctgccgt acatgcgacc tcctctttca aaagaactgt ggttttcaga tgacccaaat 600  
gtcacaaaga cactgcgatt caaacagtgg aatggaaaag agagaagcat atatttccag 660  
ccacctttct tctatgtctc tgctcaggac ctgcctcata ttgagaatgg tgggtgtggc 720  
gtcctcactg ggaagaaggc agtacagctg gatgtgagag acaacatggg gaaacttaat 780  
gatggctctc aaataacctc tgaaaagtgc ttgattgcaa caggaggtag tccaagaagt 840  
ctgtctgcca ttgatagggc tggagcagag gtgaagagta gaacaacgct tttcagaaa 900  
attggagact ttagaagctt ggagaagatt tcacgggaag tcaaatcaat tacgattatc 960  
ggtgggggct tccttggttag cgaactggcc tgtgctcttg gcagaaaggc tcgagccttg 1020  
ggcacagaag tgattcaact cttccccgag aaaggaaaata tgggaaagat cctccccgaa 1080  
tacctcagca actggaccat ggaaaaagtc agacgagagg ggggttaagg ttatcaagct 1140  
gctattgtgc aatccgttgg agtcagcagt ggcaagttac ttatcaagct gaaagacggc 1200  
aggaaggtag aaactgacca catagtggca gctgtgggcc tggagcccaa tgttgagtgt 1260  
gccaagactg gtggcctgga aatagactca gattttgggt gcttccgggt aaatgcagag 1320  
ctacaagcac gctctaactc ctgggtggca ggagatgctg catgcttcta cgaataaag 1380  
ttgggaaggc ggcggttaga gcaccatgat cacgctgttg tgagtggaaag attggctgga 1440  
gaaaatatga ctggagctgc taagccgtac tggcatcagt caatgttctg gagtgtttg 1500  
ggccccgatg ttggctatga agctatttgt cttgtggaca gtagtttggc cacagtgggt 1560  
gtttttgcaa aagcaactgc acaagacaac cccaaatctg ccacagagca gtcaggaact 1620  
ggatccgatg cagagagtgc gacagagtcc gaggcctcag aaattactat tcctcccagc 1680  
accccgagcag ttccacaggc tcccgtccag ggggaggact acggcaaggg tgtcatcttc 1740  
tacctcaggg acaaagtggc cgtggggatt gtgctatgga acatctttaa ccgaatgcca 1800  
atagcaaggc agatcattaa ggacggtgag cagcatgaag atctcaatga agtagccaaa 1860  
ctattcaaca ttcatgaaga ctgaagcccc acagtggaaat tggcaa 1906

<210> 204  
<211> 613  
<212> PRT  
<213> Homo sapiens

<400> 204  
Met Phe Arg Cys Gly Gly Leu Ala Ala Gly Ala Leu Lys Gln Lys Leu  
1 5 10 15  
Val Pro Leu Val Arg Thr Val Cys Val Arg Ser Pro Arg Gln Arg Asn  
20 25 30  
Arg Leu Pro Gly Asn Leu Phe Gln Arg Trp His Val Pro Leu Glu Leu  
35 40 45  
Gln Met Thr Arg Gln Met Ala Ser Ser Gly Ala Ser Gly Gly Lys Ile  
50 55 60  
Asp Asn Ser Val Leu Val Leu Ile Val Gly Leu Ser Thr Val Gly Ala  
65 70 75 80

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Gly Ala Tyr Ala Tyr Lys Thr Met Lys Glu Asp Glu Lys Arg Tyr Asn
85 90 95
Glu Arg Ile Ser Gly Leu Gly Leu Thr Pro Glu Gln Lys Gln Lys Lys
100 105 110
Ala Ala Leu Ser Ala Ser Glu Gly Glu Glu Val Pro Gln Asp Lys Ala
115 120 125
Pro Ser His Val Pro Phe Leu Ile Gly Gly Gly Thr Ala Ala Phe
130 135 140
Ala Ala Ala Arg Ser Ile Arg Ala Arg Asp Pro Gly Ala Arg Val Leu
145 150 155 160
Ile Val Ser Glu Asp Pro Glu Leu Pro Tyr Met Arg Pro Pro Leu Ser
165 170 175
Lys Glu Leu Trp Phe Ser Asp Asp Pro Asn Val Thr Lys Thr Leu Arg
180 185 190
Phe Lys Gln Trp Asn Gly Lys Glu Arg Ser Ile Tyr Phe Gln Pro Pro
195 200 205
Ser Phe Tyr Val Ser Ala Gln Asp Leu Pro His Ile Glu Asn Gly Gly
210 215 220
Val Ala Val Leu Thr Gly Lys Lys Val Val Gln Leu Asp Val Arg Asp
225 230 235 240
Asn Met Val Lys Leu Asn Asp Gly Ser Gln Ile Thr Tyr Glu Lys Cys
245 250 255
Leu Ile Ala Thr Gly Gly Thr Pro Arg Ser Leu Ser Ala Ile Asp Arg
260 265 270
Ala Gly Ala Glu Val Lys Ser Arg Thr Thr Leu Phe Arg Lys Ile Gly
275 280 285
Asp Phe Arg Ser Leu Glu Lys Ile Ser Arg Glu Val Lys Ser Ile Thr
290 295 300
Ile Ile Gly Gly Gly Phe Leu Gly Ser Glu Leu Ala Cys Ala Leu Gly
305 310 315 320
Arg Lys Ala Arg Ala Leu Gly Thr Glu Val Ile Gln Leu Phe Pro Glu
325 330 335
Lys Gly Asn Met Gly Lys Ile Leu Pro Glu Tyr Leu Ser Asn Trp Thr
340 345 350
Met Glu Lys Val Arg Arg Glu Gly Val Lys Val Met Pro Asn Ala Ile
355 360 365
Val Gln Ser Val Gly Val Ser Ser Gly Lys Leu Leu Ile Lys Leu Lys
370 375 380
Asp Gly Arg Lys Val Glu Thr Asp His Ile Val Ala Ala Val Gly Leu
385 390 395 400
Glu Pro Asn Val Glu Leu Ala Lys Thr Gly Gly Leu Glu Ile Asp Ser
405 410 415
Asp Phe Gly Gly Phe Arg Val Asn Ala Glu Leu Gln Ala Arg Ser Asn
420 425 430
Ile Trp Val Ala Gly Asp Ala Ala Cys Phe Tyr Asp Ile Lys Leu Gly
435 440 445
Arg Arg Arg Val Glu His His Asp His Ala Val Val Ser Gly Arg Leu
450 455 460
Ala Gly Glu Asn Met Thr Gly Ala Ala Lys Pro Tyr Trp His Gln Ser
465 470 475 480
Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly Tyr Glu Ala Ile Gly
485 490 495
Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val Phe Ala Lys Ala Thr
500 505 510
Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln Ser Gly Thr Gly Ile
515 520 525
Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser Glu Ile Thr Ile Pro
530 535 540
Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val Gln Gly Glu Asp Tyr
545 550 555 560
Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys Val Val Val Gly Ile
565 570 575
Val Leu Trp Asn Ile Phe Asn Arg Met Ile Ala Arg Lys Ile Ile
580 585 590
Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu Val Ala Lys Leu Phe
595 600 605
Asn Ile His Glu Asp
610

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<210> 205  
<211> 1090  
<212> DNA  
<213> Homo sapiens

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<400> 205
atggccgctg acaggggacg caggatattg ggagtgtgtg gcatgcatcc tcatcatcag 60
gaaactctaa aaaagaaccg agtgggtgcta gccaaacagc tgttgttgag cgaattgtta 120
gaacatcttc tggagaagga catcatcacc ttggaaatga gggagctcat ccaggccaaa 180
gtgggcagtt tcagccagaa tgtggaactc ctcaacttgc tgcctaagag ggggtcccaa 240
gcttttgatg ccttctgtga agccttgac tcctgaattt tatcaaacac acttcagct 300
ggcatatagg ttgcagtctc ggcctcgtgg cctagcactg gtgttgagca atgtgcactt 360
cactggagag aaagaactgg aatttcgctc tggaggggat gtggaccaca gtactctagt 420
caccctcttc aagcttttgg gctatgacgt ccatgttcta tgtgaccaga ctgcacagga 480
aatgcaagag aaactgcaga attttgcaca gttacctgca caccgagtc cggactgctg 540
catcgtggca ctctctcgc atgggtgtgga gggcgccatc tatggtgtgg atgggaaact 600
gctccagctc caagaggttt ttcagctctt tgacaacgcc aaccgcccaa gcctacagaa 660
caaaccacaa atgttcttca tccaggcctg ccgtggagat gagactaatc gtgggggtta 720
ccaacaagat ggaaaagaacc acgcaggatc ccctgggtgc gaggagagtg atgccggtta 780
agaaaagtgt ccgaagatga gactgcccac gcgctcagac atgatatgcg gctatgcctg 840
cctcaaaggg actgccgcca tgcggaacac caaacgaggt tcttggtaca tcgaggctct 900
tgctcaagtg ttttctgagc gggcttgtga tatgcacgtg gccgacatgc tgggttaagg 960
gaacgcactt atcaaggatc gggaaggtaa tgctcctggc acagaattcc accggtgcaa 1020
ggagatgtct gaatactgca gcactctgtg ccgccacctc tacctgttcc caggacacct 1080
tcccacatga                                     1090

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<210> 206  
<211> 91  
<212> PRT  
<213> Homo sapiens

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<400> 206
Met Ala Ala Asp Arg Gly Arg Arg Ile Leu Gly Val Cys Gly Met His
 1      5      10      15
Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala Lys
 20      25      30
Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp Ile
 35      40      45
Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly Ser Phe
 50      55      60
Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro Gln
 65      70      75      80
Ala Phe Asp Ala Phe Cys Glu Ala Leu His Ser
      85      90

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<210> 207  
<211> 714  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

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<400> 207
tctgatcagg agcccaaata ttgtgacaaa actcacacat gccaccgtg cccagcacct 60
gaactccttg ggggaccgtc agtcttcttc ttcccccaa aaccacagga caccctcatg 120
atctcccgga ccctgaggtt cacatgcgtg gtggtggacg tgagccacga agaccctgag 180
gtcaagtcca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgagg 240
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 300
tggctgaatg gcaaggagta caagtgcagg gtctccaaca aagccctccc agccccatc 360
gagaaaacaa tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 420
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 480
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 540
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 600
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 660
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgatc taga 714

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<210> 208  
<211> 235  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 208  
Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro  
1 5 10 15  
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
20 25 30  
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
35 40 45  
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
50 55 60  
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
65 70 75 80  
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
85 90 95  
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
100 105 110  
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
115 120 125  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
130 135 140  
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
145 150 155 160  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
165 170 175  
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
180 185 190  
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
195 200 205  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
210 215 220  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230 235

<210> 209  
<211> 718  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<221> misc\_feature  
<222> 34, 43, 52, 55, 58, 64  
<223> n = A,T,C or G

<400> 209  
tgatcaagaa ccacatggag gatgcacgtg cccncagtgc ccncaatgcc cngcncnga 60  
actnccagga ggcccttctg tctttgtctt ccccccga aa tcctctccat 120  
ttttggaggc cgagtcacgt gcgttgtagt ggacgtcgga aagaaagacc ccgaggtcaa 180  
tttcaactgg tatattgatg gcgttgaggt gcgaacggcc aatacgaagc caaaagagga 240  
acagttcaac agcacgtacc gcgtggtcag cgtcctgccc atccagcacc aggactggct 300  
gacggggaag gaattcaagt gcaaggtcaa caacaaagct ctcccggccc ccatcgagag 360  
gaccatctcc aaggccaaag ggcagaccgc ggagccgcag gtgtacaccc tggccccaca 420  
ccgggaagaa ctggccaagg acaccgtgag cgtaacatgc ctgggtcaaag gcttctaccc 480  
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc 540  
caacacgccc ccacagctgg acaacgacgg gacctacttc ctctacagca agctctcggg 600  
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtgggtgatgc atgaggccct 660  
gcacaaccac tacaccaga aatccatcac ccagtcttcg ggtaaatagt aatctaga 718

<210> 210  
<211> 757

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Fusion polynucleotide

&lt;400&gt; 210

tgatcaagaa	cccaagacac	caaaaccaca	accacaa cca	caaccacaac	ccaatcctac	60
aacagaatcc	aagtgtccca	aatgtccagc	ccctgagctc	ctgggagggc	cctcagtctt	120
catcttcccc	ccgaaaccca	aggacgtcct	ctccatttct	gggaggcccg	aggtcacgtg	180
cgttggtgta	gacgtgggcc	aggaagaccc	cgaggtcagt	ttcaactggg	acattgatgg	240
cgctgaggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgtaccg	300
cggtgtcagc	gtcctgcccc	tccagcacca	ggactggctg	acggggaagg	aattcaagtg	360
caaggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagaccggg	gagccgcagg	tgtacaccct	ggcccca cac	cggaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tggtcaaagg	cttctaccca	cctgatatca	acgttgagtg	540
gcagaggaat	gggcagccgg	agtcagaggg	cacytacgcc	accacgccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	tggtgatgca	cgaggccctg	cacaaccact	acaccagaa	720
atccatcacc	cagtcttcgg	gtaaatagta	atctaga			757

&lt;210&gt; 211

&lt;211&gt; 727

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Fusion polynucleotide

&lt;400&gt; 211

tgatcaagcg	caccacagcg	aagaccccg	ctccaagtgt	cccaaatgcc	caggccctga	60
actccttggg	gggcccacgg	tcttcatctt	ccccccgaaa	gccaaggacg	tcctctccat	120
cacccgaaaa	cctgaggtca	cggtgcttgg	gtggacgtgg	gtaaagaaga	ccctgagatc	180
gagttcaagc	tggtccgtgg	atgacacaga	ggtacacacg	gctgagacaa	agccaaagga	240
ggaacagttc	aacagcacgt	accgcgtggg	cagcgtcctg	cccattccagc	accaggactg	300
gctgacgggg	aaggaattca	agtgcagggt	caacaacaaa	gctctcccag	cccccatcga	360
gaggaccatc	tccaaggcca	aagggcagac	ccgggagccg	caggtgtaca	ccctggcccc	420
acaccgggaa	gagctggcca	aggacaccgt	gagcgttaac	tgcctggtca	aaggcttctt	480
cccagctgac	atcaacgttg	agtggcagag	gaatgggcag	ccggagtcag	agggcaccta	540
cgccaacacg	ccgccacagc	tggaacaacga	cgggacctac	ttcctctaca	gcaaactctc	600
cggtgggaaag	aacacgtggc	agcagggaga	agtcttcacc	tgtgtggtga	tgacagaggc	660
tctacacaat	cactccaccc	agaaatccat	caccagctct	tcgggtaaat	agtaatctag	720
agggcc						727

&lt;210&gt; 212

&lt;211&gt; 231

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Fusion polypeptide

&lt;400&gt; 212

Glu	Pro	His	Gly	Gly	Cys	Thr	Cys	Pro	Gln	Cys	Pro	Ala	Pro	Glu	Leu
1				5					10					15	
Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
			20					25					30		
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		35					40					45			
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
	50					55					60				
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
	65				70					75				80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
			85						90					95	
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
			100					105					110		
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
		115					120					125			

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr  
130 135 140  
Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn  
145 150 155 160  
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala  
165 170 175  
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser  
180 185 190  
Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr  
195 200 205  
Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
210 215 220  
Ile Thr Gln Ser Ser Gly Lys  
225 230

<210> 213  
<211> 248  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 213  
Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln  
1 5 10 15  
Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu  
20 25 30  
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp  
35 40 45  
Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Asp  
50 55 60  
Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly  
65 70 75 80  
Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn  
85 90 95  
Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp  
100 105 110  
Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro  
115 120 125  
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu  
130 135 140  
Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp  
145 150 155 160  
Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile  
165 170 175  
Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr  
180 185 190  
Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr  
195 200 205  
Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe  
210 215 220  
Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
225 230 235 240  
Ser Ile Thr Gln Ser Ser Gly Lys  
245

<210> 214  
<211> 236  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 214  
Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 1 5 10 15  
 Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro  
 20 25 30  
 Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys  
 35 40 45  
 Leu Trp Trp Thr Trp Val Lys Thr Leu Arg Ser Ser Ser Ser Trp  
 50 55 60  
 Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu  
 65 70 75 80  
 Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln  
 85 90 95  
 His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn  
 100 105 110  
 Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly  
 115 120 125  
 Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu  
 130 135 140  
 Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe  
 145 150 155 160  
 Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser  
 165 170 175  
 Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr  
 180 185 190  
 Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln  
 195 200 205  
 Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His  
 210 215 220  
 Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys  
 225 230 235

<210> 215  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion polynucleotide

<400> 215  
 gatcaggagc ccaaattcttg tgacaaaact cacacatgcc caCcgTgccc agca 54

<210> 216  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Fusion polypeptide

<400> 216  
 Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 1 5 10 15  
 Pro Ala

<210> 217  
 <211> 54  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Fusion polynucleotide

<400> 217  
 gatctggagc ccaaattcttg tgacaaaact cacacatgcc cacCgTgccc agca 54

<210> 218

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 218  
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
1 5 10 15  
Pro Ala

<210> 219  
<211> 327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 219  
cctgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 60  
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcca gacaaagccg 180  
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240  
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct ccagccccc 300  
atcgagaaaa ccattctcaa agccaaa 327

<210> 220  
<211> 109  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 220  
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
1 5 10 15  
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
20 25 30  
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
35 40 45  
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
50 55 60  
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
65 70 75 80  
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
85 90 95  
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
100 105

<210> 221  
<211> 324  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 221  
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aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 120  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 180  
gacggctcct tcttctctta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt 324  
ctctccctgt ccccggttaa atga

<210> 222  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 222  
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
1 5 10 15  
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
20 25 30  
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
35 40 45  
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
50 55 60  
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
65 70 75 80  
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
85 90 95  
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
100 105

<210> 223  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 223  
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<210> 224  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 224  
Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser  
1 5 10 15  
Pro Ala

<210> 225  
<211> 712  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Fusion polynucleotide

<400> 225  
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cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc aaggacacc tcatgatctc 120  
ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa 180  
gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct 300  
gaatggcaag gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa 360  
aacaatctcc aaagccaaag ggcagcccg agaaccacag gtgtacaccc tgcccccatc 420  
ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc 480  
cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac 540  
gcctcccgtg ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa 600  
gagcaggtgg cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa 660  
ccactacacg cagaagagcc tctccctgtc tccgggtaaa tgataatcta ga 712

<210> 226  
<211> 233  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Fusion polypeptide

<400> 226  
Asp His Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser  
1 5 10 15  
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
20 25 30  
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
35 40 45  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
50 55 60  
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
65 70 75 80  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
85 90 95  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
100 105 110  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
115 120 125  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
130 135 140  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
145 150 155 160  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220  
Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 227  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' primer for llama IgG1 constant region

<400> 227  
gtgttgatc aagaaccaca tggaggatgc acgtg

35

<210> 228  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> 5' primer for llama IgG2 constant region

<400> 228  
gttggtgatc aagaacccaa gacacaaaa cc 32

<210> 229  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' primer for llama IgG3 constant region

<400> 229  
gttggtgatc aagcgcacca cagcgaagac ccc 33

<210> 230  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Llama Fc sense sequencing primer

<400> 230  
ctgagatcga gtccagctg 19

<210> 231  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Llama Fc antisense sequencing primer

<400> 231  
cctcctttgg ctttgtctc 19

<210> 232  
<211> 1527  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<221> misc\_feature  
<222> 843, 852, 861, 864, 867, 873  
<223> n = A,T,C or G

<400> 232  
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gtcataattg ccagaggaca aattgtcttc tcccagcttc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctccccaaaa ccctggattt atgccccatc caacctggct 240  
tctggagtcc ctgctcgctt cagtggcagt gggtctggga cctcttactc tctcacaatc 300  
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360  
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtgggctc gggcggtggg 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgctg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780  
ggcacaggga ccacgggtcac cgtctcttct gatcaagaac cacatggagg atgcacgtgc 840

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 gacgtcggaa agaaagacc cgaggtcaat ttcaactggt atattgatgg cgttgaagg 1020  
 cgaacggcca atacgaagcc aaaagaggaa cagttcaaca gcacgtaccg cgttgtcagc 1080  
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 aacaaagctc tcccggcccc catcgagagg accatctcca aggccaaagg gcagacccgg 1200  
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 ggtagcggg agtcagaggg cacctacgcc aacacgccgc cacagctgga caacgaagg 1380  
 acctacttcc tctacagcaa gctctcggtg ggaaagaaca cgtggcagcg gggagaacc 1440  
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 cagtcttcgg gtaaatagta atctaga 1527

<210> 233  
 <211> 1566  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 233  
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 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240  
 tctggagtcct ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420  
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggg 480  
 aggcctgggg cctcagtga gatgtcctgc aaggctctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaatag gtgatacttc ctacaatcag aagttaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggctact cgatgtctgg 780  
 ggcacaggga ccacggtcac cgtctcttct gatcaagaac ccaagacacc aaaacca 840  
 ccacaaccac aaccacaacc caatctaca acagaatcca agtgtcccaa atgtccagcc 900  
 cctgagctcc tgggagggcc ctcagctctc atcttcccc cgaaccccaa ggacgtctc 960  
 tccatttctg ggaggccga ggtcacgtgc gctgggctgg aatggattgg ggaagacccc 1020  
 gaggtcagtt tcaactggta cattgatggc cctgaggtgc gaacggccaa cagcaggcca 1080  
 aaagaggaac agttcaacag caggtaccgc gtggtcagcg tcctgcccac ccagcacca 1140  
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 atcgagaaga ccatctccaa ggccaaaggg cagacccggg agccgcaggt gtacaccctg 1260  
 gccccacacc ggggaagagct ggccaaaggac accgtgagcg taacatgcct ggtcaaaagg 1320  
 ttctacccac ctgatataca cgttgagtgg cagaggaatg ggcagccgga gtcagaggc 1380  
 acytacgcca ccacgccacc ccagctggag aacgacggga cctacttcct ctacagcaag 1440  
 ctctcggtgg gaaagaacac gtggcagcag ggagaaacct tcacctgtgt ggtgatgac 1500  
 gaggccctgc acaaccacta caccagaaa tccatcacc agtcttcggg taaatagtaa 1566  
 tctaga 1566

<210> 234  
 <211> 1536  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 234  
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 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240  
 tctggagtcct ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420  
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggg 480  
 aggcctgggg cctcagtga gatgtcctgc aaggctctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600

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gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacagggg ccacgggtcac cgtctcttct gatcaagcga accacagcga agaccccagc 840
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ccccgaaag ccaaggacgt cctctccatc acccgaaaac ctgaggtcac gtgcttgtgg 960
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gtacacacgg ctgagacaaa gccaaaggag gaacagtcca acagcacgta ccgcgtgggtc 1080
agcgtcctgc ccattccagc ccaggactgg ctgacgggga aggaattcaa gtgcaagggtc 1140
aacaacaaag ctctcccagc ccccatcgag aggaccatct ccaaggccaa agggcagacc 1200
cgggagccgc aggtgtacac cctggcccca caccgggaag agctggccaa ggacaccgtg 1260
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aatgggcagc cggagtcaga gggcacctac gccaacacgc cgccacagct ggacaacgac 1380
gggacctact tcctctacag caaactctcc gtgggaaaga acacgtggca gcaggagaga 1440
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accagtctt cgggtaaata gtaatctaga gggccc 1536
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<210> 235

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 235

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20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175     180
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
185     190     195
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
200     205     210
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
215     220     225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
230     235     240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro His Gly
260     265     270
Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu Pro Gly Gly Pro
275     280     285
Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val Leu Ser Ile Phe
290     295     300
Gly Gly Arg Val Thr Cys Val Val Val Asp Val Gly Lys Lys Asp Pro
305     310     315     320
Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val Glu Val Arg Thr Ala
325     330     335
Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
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 340 345 350  
 Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Thr Gly Lys Glu Phe  
 355 360 365  
 Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr  
 370 375 380  
 Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu  
 385 390 400  
 Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr Val Ser Val Thr Cys  
 405 410 415  
 Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn Val Glu Trp Gln Arg  
 420 425 430  
 Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala Asn Thr Pro Gln  
 435 440 445  
 Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly  
 450 455 460  
 Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr Cys Val Val Met His  
 465 470 475 480  
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Thr Gln Ser Ser  
 485 490 495  
 Gly Lys

<210> 236  
 <211> 514  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 236  
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 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Thr  
 260 265 270  
 Pro Lys Pro Gln Pro Gln Pro Gln Pro Asn Pro Thr Thr Glu  
 275 280 285  
 Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

290	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Ser	Ile	Ser	Gly
305	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Gly	Gln	Glu	Asp	Pro
	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Ala	Glu	Val	Arg	Thr	Ala
	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe
	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
385	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr	Val	Ser	Val	Thr	Cys
	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	Asp	Ile	Asn	Val	Glu	Trp	Gln	Arg
	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala	Thr	Thr	Pro	Pro	Gln
	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Gly
465	Lys	Asn	Thr	Trp	Gln	Gln	Gly	Glu	Thr	Phe	Thr	Cys	Val	Val	Met	His
	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Ile	Thr	Gln	Ser	Ser
	Gly	Lys														

<210> 237  
<211> 503  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 237

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			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135					140				
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
		180						185					190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195					200					205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
      245
Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Ala His Ser His
      250
Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys Pro Gly Pro Glu Leu
      255
Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro Lys Ala Lys Asp Val
      260
Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys Leu Trp Trp Thr Trp
      265
Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp Ser Val Asp Asp Thr
      270
Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
      275
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
      280
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
      285
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
      290
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
      295
Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe Pro Ala Asp Ile Asn
      300
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
      305
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
      310
Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Val Phe Thr
      315
Cys Val Val Met His Glu Ala Leu His Asn His Ser Thr Gln Lys Ser
      320
Ile Thr Gln Ser Ser Gly Lys
      325
      330
      335
      340
      345
      350
      355
      360
      365
      370
      375
      380
      385
      390
      395
      400
      405
      410
      415
      420
      425
      430
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      475
      480
      485
      490
      495
      500

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<210> 238
<211> 42
<212> DNA
<213> Artificial Sequence

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<220>
<223> 3'-primer for llama IgG1, IgG2, IgG3 constant
      region

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<400> 238
gtgttttcta gattactatt tacccgaaga ctgggtgatg ga

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42

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<210> 239
<211> 1521
<212> DNA
<213> Artificial Sequence

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<220>
<223> fusion polynucleotide

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<400> 239
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtttca 60
gtcataattg ccagaggaca aattgttctc tcccagtcct cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactgtg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctgggt 240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccac 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gagtgaggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
aggcctgggg cctcagtgaat gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact ggttaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta 660

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactcttg tgacaaaact 840  
cacacatgcc caccgtgccc agcacctgaa ctctctgggg gaccgtcagt cttcctcttc 900  
ccccaaaaac ccaaggacac cctcatgata tcccggaccc ctgaggtcac atgcgtgggtg 960  
gtggacgtga gccacgaaga ccctgagggtc aagtccaact ggtacgtgga cggcgtggag 1020  
gtgcataatg ccaagacaaa gccgcgggag gaggcagtag acagcacgta ccgtgtgggtc 1080  
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140  
tccaacaaag cctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc 1260  
agcgtgacct gcctgggtcaa aggccttctat cccagcgaca tcgcccgtgga gtggggagagc 1320  
aatgggcagc cggagaacaa ctacaagacc agcgtctccg tgctggactc cgacgggtcc 1380  
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500  
tctccgggta aatgatctag a 1521

<210> 240

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 240

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
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Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70					75					80	
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
			85						90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100				105						110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115				120						125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135					140				
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
		180						185					190		
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
		195				200						205			
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225				230					235					240	
Ala	Arg	Val	Val	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	
			245					250					255		
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Asp	Gln	Glu	Pro	Lys	Ser
			260					265					270		
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
		275				280						285			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
	290					295					300				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
305					310				315					320	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
			325					330					335		
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
			340					345					350		

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
355 360 365  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
370 375 380  
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
385 390 395 400  
Val Tyr Thr Leu Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
405 410 415  
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
420 425 430  
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
435 440 445  
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
450 455 460  
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
465 470 475 480  
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
485 490 495  
Ser Pro Gly Lys  
500

<210> 241  
<211> 162  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 241  
gcggatcctt cgaacctgct cccatcctgg gccattacct taatctcagt aaatggaatt 60  
tttgtgatat gctgcctgac ctactgcttt gccccaagat gcagagagag aaggaggaat 120  
gagagattga gaagggaag tgtacgcct gtataaatcg at 162

<210> 242  
<211> 51  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 242  
Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser  
1 5 10 15  
Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro  
20 25 30  
Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val  
35 40 45  
Arg Pro Val  
50

<210> 243  
<211> 399  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 243  
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgcc ttcagtcata 60  
atgtccagag gagtgcacat tgttctgact cagctctccag ccacctgtc tgtgactcca 120  
ggagatagag tctctcttcc ctgcagggcc agccagagta ttagcgacta cttacactgg 180  
tatcaacaaa aatcacatga gtctccaagg ctctcatca aatatgttcc ccattccatc 240  
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300  
aacagtgtgg aacctgaaga tggttgaatt tattactgtc aacatggtca cagctttccg 360



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
tggacgttcg gtggaggcac caagctggaa atcaaacgg 399

<210> 244  
<211> 131  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 244  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala  
35 40 45  
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His  
50 55 60  
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu  
85 90 95  
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln  
100 105 110  
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg  
130

<210> 245  
<211> 368  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 245  
cagatccagt tgggtgcaatc tggacctgag ctgaagaagc ctggagagac agtcaggatc 60  
tcttgcaagg cttctgggta tgccttcaca actactggaa tgcagtgggt gcaagagatg 120  
ccaggaaagg gtttgaagtg gattggctgg ataaacaccc cactctggag tgccaaaata 180  
tgtagaagac ttcaaggacg gtttgccttc tctttggaaa cctctgcaa cactgcatat 240  
ttacagataa gcaacctcaa agatgaggac acggctacgt atttctgtgt gagatccggg 300  
aatggtaact atgacctggc ctactttgct tactggggcc aaggagacact ggtcactgtc 360  
tctgatca 368

<210> 246  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 246  
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15  
Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr  
20 25 30  
Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile  
35 40 45  
Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu  
50 55 60  
Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr  
65 70 75 80  
Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp  
100 105 110  
Gly Gln Gly Thr Leu Val Thr Val Ser  
115 120

<210> 247  
<211> 812  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 247  
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60  
atgtccagag gaggcgacat tgttctgact cagtctccag ccaccctgtc tgtgactcca 120  
ggagatagag tctctctttc ctgcagggcc agccagagta ttagcgacta cttacactgg 180  
tatcaacaaa aatcacatga gtctccaagg ctctcatca aatatgcttc ccattccatc 240  
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300  
aacagtgtgg aacctaaga tgggtgaatt tattactgtc aacatgggtc cagctttccg 360  
tggacgttcg gtggaggcac caagctggaa atcaaacggg gtggcgggtg ctcgggcgga 420  
gggtgggtcgg gtggcgggcg atctcagatc cagttgggtg aatctggacc tgagctgaag 480  
aagcctggag agacagtcag gatctcctgc aaggcttctg ggtatgcctt cacaactact 540  
ggaatgcagt ggggtcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600  
acccactct ggagtgccaa aatatgtaga agacttcaag gacggtttgc cttctctttg 660  
gaaacctctg ccaacactgc atatttacag ataagcaacc tcaaagatga ggacacggct 720  
acgtatttct gtgtgagatc cggaatgggt aactatgacc tggcctactt tgcttactgg 780  
ggccaaggga cactggtcac tgtctctgat ca 812

<210> 248  
<211> 267  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 248  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala  
35 40 45  
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His  
50 55 60  
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu  
85 90 95  
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln  
100 105 110  
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro  
145 150 155  
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr  
160 165 170 175  
Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys  
180 185 190  
Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg  
195 200 205  
Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr  
210 215 220  
Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr  
225 230 235 240

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala  
245 250 255  
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val ser  
260 265

<210> 249  
<211> 405  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 249  
atggattttc aagtcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60  
agaggagtcg acattgtgct cacccaatct ccagcttctt tggctgtgtc tctagggtcag 120  
agagccacca tctcctgcag agccagtgaag agtggtgaat attatgtcac aagtttaatg 180  
cagtggtacc aacagaaacc aggacagcca cccaaactcc tcactctctg tgcattcaac 240  
gtagaatctg gggtcctgc caggtttagt ggcagtgggt ctgggacaga cttcagcctc 300  
aacatccatc ctgtggagga ggatgatatt gcaatgtatt tctgtcagca aagtaggaag 360  
gttccttggg cggtcgttg aggaccaag ctggaataca aacgg 405

<210> 250  
<211> 135  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 250  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
35 40 45  
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
50 55 60  
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn  
65 70 75 80  
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Thr  
85 90 95  
Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met  
100 105 110  
Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly  
115 120 125  
Thr Lys Leu Glu Ile Lys Arg  
130 135

<210> 251  
<211> 369  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 251  
cagggtcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60  
acatgcaccg tctcagggtt ctcattaacc ggctatgggt taaactgggt tcgccagcct 120  
ccaggaaagg gtctggagtg gctgggaatg atatgggggt atggaagcac agactataat 180  
tcagctctca aatccagact gagcatcacc aaggacaact ccaagagcca agttttctta 240  
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgccag agatggttat 300  
agtaactttc attactatgt tatggactac tgggggtcaag gaacctcagt caccgtctcc 360  
tcagatctg 369

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 252  
<211> 121  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 252  
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln  
1 5 10 15  
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr  
20 25 30  
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45  
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys  
50 55 60  
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu  
65 70 75 80  
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala  
85 90 95  
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly  
100 105 110  
Gln Gly Thr Ser Val Thr Val Ser Ser  
115 120

<210> 253  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 253  
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtgc ttcagtcata 60  
atgtccagag gagtgcgacat tgtgctcacc caatctccag cttctttggc tgtgtctcta 120  
ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatatta tgtcacaagt 180  
ttaatgcagt ggtaccaaca gaaaccagga cagccaccca aactcctcat ctctgctgca 240  
tccaacgtag aatctggggg cctgccagg tttagtggca gtgggtctgg gacagacttc 300  
agcctcaaca tccatcctgt ggaggaggat gatattgcaa tgtatttctg tcagcaaagt 360  
aggaagggtc cttggacgtt cgggtggaggc accaagctgg aaatcaaacg ggggtggcgg 420  
ggctcgggcg gagggtgggtc gggtggcggc ggatctcagg tgcagctgaa ggagtcagga 480  
cctggcctgg tggcgccctc acagagcctg tccatcacat gcaccgtctc agggttctca 540  
ttaaccggct atggtgtaaa ctgggttcgc cagcctccag gaaaggggtc ggagtggctg 600  
ggaatgatat ggggtgatgg aagcacagac tataattcag ctctcaaadc cagactgagc 660  
atcaccaagg acaactccaa gagccaagtt ttcttaaaaa tgaacagtct gcaactgat 720  
gacacagcca gatactactg tgccagagat ggttatagta actttcatta ctatgttatg 780  
gactactggg gtcaaggaac ctcagtcacc gtctcctctg atcag 825

<210> 254  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 254  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
35 40 45  
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
50 55 60  
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn

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65	Val	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	80
				85						90						95	
	Asp	Phe	Ser	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Asp	Asp	Ile	Ala	Met	
				100					105					110			
	Tyr	Phe	Cys	Gln	Gln	Ser	Arg	Lys	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	
			115					120					125				
	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
			130				135					140					
	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Gly	
			145			150					155					160	
	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	
				165						170					175		
	Phe	Ser	Leu	Thr	Gly	Tyr	Gly	Val	Asn	Trp	Val	Arg	Gln	Pro	Pro	Gly	
				180					185					190			
	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Met	Ile	Trp	Gly	Asp	Gly	Ser	Thr	Asp	
			195				200						205				
	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Ser	Ile	Thr	Lys	Asp	Asn	Ser	
			210				215						220				
	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	
			225			230					235					240	
	Ala	Arg	Tyr	Tyr	Cys	Ala	Arg	Asp	Gly	Tyr	Ser	Asn	Phe	His	Tyr	Tyr	
				245						250					255		
	Val	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser		
			260						265					270			

<210> 255  
<211> 393  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 255  
atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60  
agaggagtcg acatccagat gacacagtct ccatcctcac tgtctgcatc tctgggaggc 120  
aaagtcacca tcacttgcaa ggcaagccaa gacattaaga agtatatagg ttggtaccaa 180  
cacaagcctg gaaaaggctc caggctgctc atatattaca catctacatt acagccaggc 240  
atcccatcaa ggttcagtgg aagtgggtct gggagagatt attccctcag catcagaaac 300  
ctggagcctg aagatattgc aacttattat tgtcaacagt atgataatct tccattgacg 360  
ttcggctcgg ggacaaagtt ggaaataaaa cgg 393

<210> 256  
<211> 131  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 256  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Ile Lys Arg  
130

<210> 257  
<211> 362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 257  
gatgtacagc ttcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60  
acctgctctg tcactggcta ctccatcacc agtggtttct actggaactg gatccgacag 120  
tttccgggaa acaaaactgga atggatgggc cacataagcc acgacggtag gaataactac 180  
aaccatctc tcataaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240  
ctgaagttga gttctgtgac tactgaggac acagctacat atttctgtgc aagacactac 300  
ggtagtagcg gagctatgga ctactggggt caaggaacct cagtcaccgt ctctctgat 360  
ca 362

<210> 258  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 258  
Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
1 5 10 15  
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly  
20 25 30  
Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp  
35 40 45  
Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro Ser Leu  
50 55 60  
Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe  
65 70 75 80  
Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95  
Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Ser Val Thr Val Ser Ser  
115

<210> 259  
<211> 806  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 259  
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtg cttcagtcata 60  
atgtccagag gagtcgacat ccagatgaca cagtcctcat cctcactgtc tgcattctctg 120  
ggaggcaaag tcaccatcac ttgcaaggca agccaagaca ttaagaagta tataggttgg 180  
taccaacaca agcctggaag aggtcccagg ctgctcatat attacacatc tacattacag 240  
ccaggcatcc catcaagggt cagtggaagt gggctctggga gagattattc cctcagcatc 300  
agaaacctgg agcctgaaga tattgcaact tattattgtc aacagtatga taatcttcca 360  
ttgacgttcg gctcggggac aaagtgtgaa ataaaacggg gtggcggtgg ctcgggcggt 420  
ggtgggtcgg gtggcgggcg atctgatgta cagcttcagg agtcaggacc tggcctctgtg 480  
aaaccttctc agtctctgtc tctcacctgc tctgtcactg gctactccat caccagtggg 540  
ttctactgga actggatccg acagtttccg tctctcataa ttcgaatctc catcactcgt 600  
agccacgacg gtaggaataa ctacaaccga tctctcataa atcgaatctc catcactcgt 660  
gacacatcta agaaccagtt tttcctgaag ttgagttctg tgactactga ggacacagct 720

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
acatatttct gtgcaagaca ctacgtagt agcggagcta tggactactg gggtaagga 780  
acctcagtca ccgtctcctc tgatca 806

<210> 260  
<211> 266  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 260  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
145 150 155 160  
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
165 170 175  
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
180 185 190  
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro  
195 200 205  
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
210 215 220  
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr  
225 230 235 240  
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly  
245 250 255  
Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
260 265

<210> 261  
<211> 417  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 261  
atggcatgga gctgcattat tttcttcttg gtatcagtaa ttacagggtg ccattcccag 60  
gtcaagctgc agcagtccgg ttctgaacta gggaaacctg gggcctcagt gaaactgtcc 120  
tgcaagactt caggctacat attcacagat cactatattt cttgggtgaa acagaagcct 180  
ggagaaagcc tgcagtggat aggaaatggt tatggtggaa atggtgttac aagctacaat 240  
caaaaattcc agggcaaggc cacactgact gtagataaaa tctctagcac agcctacatg 300  
gaactcagca gcctgacatc tgaggattct gccatctatt actgtgcaag aaggccggta 360  
gcgacgggcc atgctatgga ctactggggg caggggatcc aagttaccgt ctcctca 417

<210> 262  
<211> 139  
<212> PRT  
<213> Artificial Sequence

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<220>

<223> fusion polypeptide

<400> 262

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Met Ala Trp Ser Cys Ile Ile Phe Phe Leu Val Ser Val Ile Thr Gly
 1      5      10      15
Val His Ser Gln Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys
 20      25      30
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
 35      40      45
Thr Asp His Tyr Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu
 50      55      60
Gln Trp Ile Gly Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn
 65      70      75
Gln Lys Phe Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser
 85      90      95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile
100      105      110
Tyr Tyr Cys Ala Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr
115      120      125
Trp Gly Gln Gly Ile Gln Val Thr Val Ser Ser
130      135

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<210> 263

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 263

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atgttggtata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60
gacatagtgac tgactcagac tccagccact ctgtctctaa ttccctggaga aagagtcaca 120
atgacctgta agaccagtca gaattattggc acaatcttac actggtatca ccaaaaacca 180
aaggaggctc caagggtctt catcaagtat gcttcgcagt ccattcctgg gatccctcc 240
agattcagtg gcagtgggtc ggaaacagat ttcactctca gcatcaataa cctggagcct 300
gatgatatcg gaatttatta ctgtcaacaa agtagaagct ggctgtcac gttcggctct 360
ggcaccaagc tggagataaa a
381

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<210> 264

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 264

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
 1      5      10      15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
 20      25      30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35      40      45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50      55      60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65      70      75
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85      90      95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100      105      110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
115      120      125

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<210> 265  
<211> 1671  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 265  
aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtg ttcagtcata 60  
atgtccagag gagtgcacat tgttctgact cagttctccag ccaccctgtc tgtgactcca 120  
ggagatagag tctctctttc ctgcagggcc agccagagta ttagcgacta cttacactgg 180  
tatcaacaaa aatcacatga gtctccaagg cttctcatca aatatgtctc ccattccatc 240  
tctgggatcc cctccagggt cagtggcagt ggatcagggt cagatttcac tctcagtatc 300  
aacagtgtgg aacctgaaga tgttggaaatt tattactgtc aacatgggtc cagctttccg 360  
tggagcttcg gtggaggcac caagctggaa atcaaacggg gtggcggtgg ctccggcgga 420  
ggtgggtcgg gtggcggtcg atctcagatc cagttgggtg aatctggacc tgagctgaag 480  
aagcctggag agacagtcag gatctcctgc aaggcttctg ggtatgcctt cacaactact 540  
ggaatgcagt ggtgtcaaga gatgccagga aagggtttga agtggattgg ctggataaac 600  
acccactctt ggagtgccaa aatatgtaga agacttcaag gacggtttgc cttctctttg 660  
gaaacctctg ccaacactgc atattttacag ataagcaacc tcaaagatga ggacacggct 720  
acgtatttct gtgtgagatc cggaatggt aactatgacc tggcctactt tgcttactgg 780  
ggccaaggga cactgggtcac tgtctctgat ctggagccca aatcttctga caaaactcac 840  
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 900  
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 960  
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 1020  
cataatgccca agacaaagcc gcgggaggag aagtacaaca gcacgtaccg tgtggtcagc 1080  
gtcttcaccg tcttgaccca ggactggctg aatggcaagg agtacaagtg caaggctctc 1140  
aacaagagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200  
gaaccacagg tgtaaccctt gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260  
ctgacgtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320  
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380  
ttctcttaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440  
tgctccgtga tgcattgagg cctgcacaac cactacacgc agaagagcct ctccctgtct 1500  
ccgggtaaaag cggatccttc gaacctgctc ccatctggg ccattacctt aatctcagta 1560  
aatggaattt ttgtgatatg ctgcctgacc tactgctttg cccaagatg cagagagaga 1620  
aggaggaatg agagattgag aagggaaagt gtacgccttg tataaatcga t 1671

<210> 266  
<211> 552  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 266  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
20 25 30  
Thr Leu Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala  
35 40 45  
Ser Gln Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His  
50 55 60  
Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu  
85 90 95  
Ser Ile Asn Ser Val Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln  
100 105 110  
His Gly His Ser Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu  
115 120 125  
Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro  
145 150 155 160  
Gly Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr  
165 170 175

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Thr Thr Gly Met Gln Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys  
 180 185 190  
 Trp Ile Gly Trp Ile Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg  
 195 200 205  
 Arg Leu Gln Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr  
 210 215 220  
 Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr  
 225 230 235 240  
 Phe Cys Val Arg Ser Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala  
 245 250 255  
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asp Leu Glu Pro Lys  
 260 265 270  
 Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu  
 275 280 285  
 Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 290 295 300  
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 305 310 315 320  
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val  
 325 330 335  
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser  
 340 345 350  
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 355 360 365  
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala  
 370 375 380  
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 385 390 395 400  
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln  
 405 410 415  
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 420 425 430  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 435 440 445  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 450 455 460  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 465 470 475 480  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 485 490 495  
 Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala  
 500 505 510  
 Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr  
 515 520 525  
 Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu  
 530 535 540  
 Arg Arg Glu Ser Val Arg Pro Val  
 545 550

<210> 267  
 <211> 1683  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 267  
 aagcttatgg attttcaagt gcagattttc agcttcctgc taatcagtg ttcagtcata 60  
 atgtccagag gagtcgacat tgtgctcacc caatctccag cttctttggc tgtgtctcta 120  
 ggtcagagag ccaccatctc ctgcagagcc agtgaaagtg ttgaatatta tgtcacaagt 180  
 ttaatgcagt ggtaccaaca gaaaccagga cagccacca aactcctcat ctctgtgca 240  
 tccaacgtag aatctggggt ccctgccagg tttagtggca gtgggtctgg gacagacttc 300  
 agcctcaaca tccatcctgt ggaggaggat gatattgcaa tgtatttctg tcagcaaagt 360  
 aggaagggtt cttggacgtt cggtggaggc accaagctgg aaatcaaacg ggggtggcgg 420  
 ggctcgggcg gaggtggggtc gggtggcggc ggatctcagg tgcagctgaa ggagtcagga 480  
 cctggcctgg tggcgccctc acagagcctg tccatcacat gcaccgtctc agggttctca 540  
 ttaaccggct atggtgtaaa ctgggttcgc cagcctccag gaaagggctt ggagtggctg 600

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 ggaatgatata ggggtgatgg aagcacagac tataattcag ctctcaaatc cagactgagc 660  
 atcaccaagg acaactccaa gagccaagtt ttcttaaaaa tgaacagtct gcaaaactgat 720  
 gacacagcca gataactactg tgccagagat ggttatagta actttcatta ctatgttatg 780  
 gactactggg gtcaaggaac ctgagtcacc gtctcctcag atctggagcc caaatcttct 840  
 gacaaaactc acacatcccc accgtcccca gcacctgaac tcctgggggg atcgtcagtc 900  
 ttctcttctc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 960  
 tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1020  
 ggcgtggagg tgcataatgc caagacaaag ccgcggggagg agcagtacaa cagcacgtac 1080  
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1140  
 tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 1200  
 gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggatga gctgaccaag 1260  
 aaccaggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat gccgtggag 1320  
 tgggagagca atgggagacc ggagaacaac tacaagacca cgctcccgt gctggactcc 1380  
 gacggctcct tcttctctta cagcaagctc accgtggaga agagcaggtg gcagcagggg 1440  
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1500  
 ctctccctgt ctccgggtaa agcggatcct tcgaacctgc tcccatcctg gccattacc 1560  
 ttaatctcag taaatggaat ttttgtgata tgctgcctga cctactgctt tgccccaaga 1620  
 tgcagagaga gaaggaggaa tgagagattg agaagggaaa gtgtacgcc tgtataaatc 1680  
 gat 1683

<210> 268  
 <211> 556  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 268  
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 1 5 10 15  
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Ala  
 20 25 30  
 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala  
 35 40 45  
 Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln  
 50 55 60  
 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn  
 65 70 75 80  
 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 85 90 95  
 Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met  
 100 105 110  
 Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly  
 115 120 125  
 Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly  
 130 135 140  
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly  
 145 150 155 160  
 Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly  
 165 170 175  
 Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly  
 180 185 190  
 Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr Asp  
 195 200 205  
 Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser  
 210 215 220  
 Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr  
 225 230 235 240  
 Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr  
 245 250 255  
 Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp  
 260 265 270  
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro  
 275 280 285  
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys  
 290 295 300  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 305 310 315 320

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
355 360 365  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 395 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475 480  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu  
500 505 510  
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile  
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<212> DNA  
<213> Artificial sequence

<220>  
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<220>  
<223> fusion polypeptide

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Ser Leu Ser Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala  
35 40 45  
Ser Gln Asp Ile Lys Lys Tyr Ile Gly Trp Tyr Gln His Lys Pro Gly  
50 55 60  
Lys Gly Pro Arg Leu Leu Ile Tyr Tyr Thr Ser Thr Leu Gln Pro Gly  
65 70 75 80  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Leu  
85 90 95  
Ser Ile Arg Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Gln Tyr Asp Asn Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu  
115 120 125  
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130 135 140  
Gly Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro  
145 150 155 160  
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr  
165 170 175  
Ser Gly Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu  
180 185 190  
Glu Trp Met Gly His Ile Ser His Asp Gly Arg Asn Asn Tyr Asn Pro  
195 200 205  
Ser Leu Ile Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln  
210 215 220  
Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr  
225 230 235 240  
Phe Cys Ala Arg His Tyr Gly Ser Ser Gly Ala Met Asp Tyr Trp Gly  
245 250 255  
Gln Gly Thr Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser  
260 265 270  
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly  
275 280 285  
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
290 295 300  
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
305 310 315 320  
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
325 330 335  
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
340 345 350  
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
355 360 365  
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
370 375 380  
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
385 390 395 400  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
435 440 445  
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
450 455 460  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 aaggaggctc caagggtctc catcaagtat gcttcgcagt ccattcctgg gatccccctc 240  
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<210> 272  
 <211> 548  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

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 Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn  
 35 40 45  
 Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro  
 50 55 60  
 Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser

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 100 105 110  
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg  
 115 120 125  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln  
 130 135 140  
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser  
 145 150 155 160  
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr  
 165 170 175  
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly  
 180 185 190  
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln  
 195 200 205  
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met  
 210 215 220  
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala  
 225 230 235 240  
 Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly  
 245 250 255  
 Ile Gln Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys  
 260 265 270  
 Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser  
 275 280 285  
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 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
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 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
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 405 410 415  
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 420 425 430  
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu  
 435 440 445  
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
 450 455 460  
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
 465 470 475 480  
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 485 490 495  
 Lys Ala Asp Pro Ser Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile  
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 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala  
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<210> 273  
 <211> 1521  
 <212> DNA  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> fusion polynucleotide

<400> 273

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<210> 274

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 274

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35     40     45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50     55     60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65     70     75     80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85     90     95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100    105    110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115    120    125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130    135    140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145    150    155    160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165    170    175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180    185    190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195    200    205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210    215    220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225    230    235    240

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<400> 277
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<210> 278
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<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to amplify constant regions for creating
      IgG hinge mutants

<400> 278
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<210> 279
<211> 56
<212> DNA
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<220>
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<211> 30
<212> DNA
<213> Artificial Sequence

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<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

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<400> 281
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<210> 282
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo for second PCR to insert IgA hinge into
      fused to IgG1 CH2

<400> 282
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<210> 283
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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<210> 284  
<211> 505  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

Gly	Thr	Gly	Thr	Val	Thr	Val	Ser	Asp	Gln	Pro	Val	Pro	Ser	Thr
Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Cys
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Lys
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Tyr
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	His
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Lys
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gln
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Leu
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Pro
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Leu
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Val
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Gln
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						

<210> 285  
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<220>  
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<400> 285

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ccaggggaga	aggtcacaat	gacttgacag	gccagctcaa	gtgtaagta	catgcactgg	180
taccagcaga	agccaggatc	ctccccaaa	ccctggattt	atgccccatc	caacctggct	240
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agcagagtgg	aggctgaaga	tgctgccact	tattactgcc	agcagtggag	ttttaaccca	360
cccacgttcg	gtgctgggac	caagctggag	ctgaaaagatg	gcggtggctc	ggcggtggtg	420
ggatctggag	gaggtgggag	ctctcaggct	tatctacagc	agtctggggc	tgagctgggtg	480
aggcctgggg	cctcagtga	gatgtcctgc	aaggctctcg	gctacacatt	taccagttac	540
aatatgcact	gggtaaagca	gacacctaga	cagggcctgg	aatggattgg	agctatttat	600
ccaggaatg	gtgatacttc	ctacaatcag	aagttcaagg	gcaaggccac	actgactgta	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctcg	720
gtctatttct	gtgcaagagt	gggtacttat	agtaactctt	actggtactt	cgatgtctgg	780
ggcacagggg	ccacggtcac	cgctctctct	gatcagccag	ttccctcaac	tccacctacc	840
ccatctccct	caactccacc	tacctcatct	ccctcatgct	gccacccccg	actgtcactg	900
caccgaccgg	ccctcgagga	cctgctctta	gggttcagaag	cgatcctcac	gtgcacactg	960
accggcctga	gagatgcctc	agggtgcacc	ttcacctgga	cgccctcaag	tggaagagac	1020
gctgttcaag	gaccacctga	ccgtgacctc	tgtggctgct	acagcgtgtc	cagtgtcctg	1080
ccgggctgtg	ccgagccatg	gaaccatggg	aagacccttca	cttgactgct	tgccctaccc	1140
gagtcacaaga	ccccgctaac	cgccaccctc	tcaaaatccg	gaaacacatt	ccggccccgag	1200
gtccacctgc	tgccgcccgc	gtcggaggag	ctggccctga	acgagctggt	gacgtgacg	1260
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gagctgcccc	gcgagaagta	cctgacttgg	gcattccccgc	aggagcccag	ccagggcacc	1380
accaccttcg	ctgtgaccag	catactgcgc	gtggcagccg	aggactggaa	gaagggggac	1440
accttctcct	gcatgggtgg	ccacgaggcc	ctgccgctgg	ccttcacaca	gaagaccatc	1500

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<210> 286  
<211> 520  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 286  
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20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Leu Lys  
115 120 125  
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser  
260 265 270  
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Ser  
275 280 285  
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu  
290 295 300  
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg  
305 310 315 320  
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser  
325 330 335  
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val  
340 345 350  
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr  
355 360 365  
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala  
370 375 380  
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu  
385 390 395 400  
Pro Pro Pro Ser Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr  
405 410 415  
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu  
420 425 430  
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser  
435 440 445  
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile

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49076.000004pct2\_10.207.655 Seq List Text 07.24.03.txt  
 450 455 460  
 Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys  
 465 470 475 480  
 Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
 485 490 495  
 Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Met  
 500 505 510  
 Ala Glu Val Asp Gly Thr Cys Tyr  
 515 520

<210> 287  
 <211> 775  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 287  
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 tccctcatgc tgcaccccc gactgtcact gcaccgaccg gccctcgagg acctgtcttt 120  
 aggttcagaa gcgacacctc cgtgcacact gaccggcctg agagatgcct caggtgtcac 180  
 ctccacctgg acgcccctca gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240  
 ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300  
 gaagaccttc acttgacctg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360  
 ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga 420  
 gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gcccgaagga 480  
 tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540  
 ggcatcccgg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600  
 cgtggcagcc gaggactgga agaaggggga cactttctcc tgcattggtg gccacgaggg 660  
 cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaac ccaccatgt 720  
 caatgtgtct gttgtcatgg cggaggtgga cggcacctgc tactgataat ctaga 775

<210> 288  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 288  
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 Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg  
 20 25 30  
 Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys  
 35 40 45  
 Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr  
 50 55 60  
 Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu  
 65 70 75 80  
 Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro  
 85 90 95  
 Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser  
 100 105 110  
 Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg  
 115 120 125  
 Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn  
 130 135 140  
 Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp  
 145 150 155 160  
 Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys  
 165 170 175  
 Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr  
 180 185 190  
 Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys  
 195 200 205

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala  
210 215 220  
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val  
225 230 235 240  
Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr  
245 250

<210> 289  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to PCR IgA hinge-CH2 CH3

<400> 289  
gttgtttcta gattatcagt agcagggtgcc gtccacctcc gccatgacaa c 51

<210> 290  
<211> 429  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 290  
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acttccagga tcattcgttc ttccgaagat cctaattgagg acattgtgga gagaaacatc 120  
cgaattattg ttctcttgaa caacagggag aatatctctg atcccacctc accattgaga 180  
accagatttg tgtaccattt gtctgacctc agctgtaaaa aatgtgatcc tacagaagtg 240  
gagctggata atcagatagt tactgctacc cagagcaata tctgtgatga agacagtgtc 300  
acagagacct gctacactta tgacagaaac aagtgtctaca cagctgtggt cccactcgta 360  
tatggtggtg agacaaaat ggtggaaaca gccttaacctc cagatgcctg ctatcctgac 420  
taatctaga 429

<210> 291  
<211> 139  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 291  
Arg Ser Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys  
1 5 10 15  
Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn  
20 25 30  
Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn  
35 40 45  
Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val  
50 55 60  
Tyr His Leu Ser Asp Leu Ser Cys Lys Lys Cys Asp Pro Thr Glu Val  
65 70 75 80  
Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp  
85 90 95  
Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys  
100 105 110  
Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val  
115 120 125  
Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro  
130 135

<210> 292  
<211> 36  
<212> DNA

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<213> Artificial Sequence

<220>

<223> 5' oligo to PCR J chain

<400> 292

gttgtagat ctcaagaaga tgaaaggatt gttctt 36

<210> 293

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to PCR J chain

<400> 293

gttgtttcta gattagtcag gatagcaggc atctgg 36

<210> 294

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> 4 carboxy terminal amino acids deleted from IgA  
CH3

<400> 294

Gly Thr Cys Tyr  
1

<210> 295

<211> 763

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 295

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aggttcagaa	gcgatcctca	cgtgcacact	gaccggcctg	agagatgcct	caggtgtcac	180
cttcacctgg	acgccctcaa	gtgggaagag	cgctgttcaa	ggaccacctg	accgtgacct	240
ctgtggctgc	tacagcgtgt	ccagtgtcct	gccgggctgt	gccgagccat	ggaaccatgg	300
gaagaccttc	acttgactg	ctgcctaccc	cgagtccaag	accccgctaa	ccgccaccct	360
ctcaaaatcc	ggaaacacat	tccggcccga	ggtccacctg	ctgccgccgc	cgtcggagga	420
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tgtgctggtt	cgctggctgc	aggggtcaca	ggagctgccc	cgcgagaagt	acctgacttg	540
ggcatcccgg	caggagccca	gccagggcac	caccaccttc	gctgtgacca	gcatactgcg	600
cgtggcagcc	gaggactgga	agaaggggga	caccttctcc	tgcatgggtg	gccacgaggc	660
cctgccgctg	gccttcacac	agaagaccat	cgaccgcttg	gcgggtaaac	ccaccatgt	720
caatgtgtct	gttgtcatgg	cggaggtgga	ctgataatct	aga		763

<210> 296

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 296

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Pro	Thr	Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu	Ser	Leu	His	Arg
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Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr  
50 55 60  
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu  
65 70 75 80  
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro  
85 90 95  
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser  
100 105 110  
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg  
115 120 125  
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn  
130 135 140  
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp  
145 150 155 160  
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys  
165 170 175  
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr  
180 185 190  
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys  
195 200 205  
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala  
210 215 220  
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val  
225 230 235 240  
Asn Val Ser Val Val Met Ala Glu Val Asp  
245 250

<210> 297  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo for construct with 4 amino acid deletion  
in IgA CH3

<400> 297  
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45

<210> 298  
<211> 1572  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 298  
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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240  
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cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420  
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aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctcagcagc tgacatctga agactctgcg 720  
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caccgaccgg ccctcgagga cctgtcttta gttcagaag cgatcctcac tgggaagagc 960  
accggtctga gagatgcctc aggtgtcacc ttacactgga cgccctcaag tgggaagagc 1020  
gctgttcaag gaccactga ccgtgacctc tgtggctgct acagcgtgtc cagtgtcctg 1080

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 gaggccaaga ccccgctaac cgccaccctc tcaaaatccg gaaacacatt ccggccccgag 1200  
 gtccacctgc tgccgccgcc gtcggaggag ctggccctga acgagctggt gacgctgacg 1260  
 tgcttggcac gtggcttcag cccaaggat gtgctgggtc gctggctgca ggggtcacag 1320  
 gagctgcccc gcgagaagta cctgacttgg gcatcccggc aggagcccag ccagggcacc 1380  
 accaccttcg ctgtgaccag catactgctc gtggcagccg aggactggaa gaagggggac 1440  
 accttctcct gcatgggtgg ccacgagggc ctgccgctgg ccttcacaca gaagaccatc 1500  
 gaccgcttgg cgggtaaac caccatgtc aatgtgtctg ttgtcatggc ggaggtggac 1560  
 tgataatcta ga 1572

<210> 299  
 <211> 516  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 299  
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 1 5 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser  
 260 265 270  
 Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser  
 275 280 285  
 Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu  
 290 295 300  
 Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg  
 305 310 315 320  
 Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser  
 325 330 335  
 Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val  
 340 345 350  
 Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr  
 355 360 365  
 Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala  
 370 375 380  
 Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu  
 385 390 395 400

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr  
405 410 415  
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu  
420 425 430  
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser  
435 440 445  
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile  
450 455 460  
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys  
465 470 475 480  
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
485 490 495  
Asp Arg Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met  
500 505 510  
Ala Glu Val Asp  
515

<210> 300  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> 14 amino acids deleted from IgAH-T4 (so that total  
of 18 amino acids deleted from wild type IgA CH3

<400> 300  
Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp  
1 5 10

<210> 301  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo for engineering 14 amino acid from IgA-T4

<400> 301  
gttggtttcta gattatcatt taccgcgcaa gcggtcgatg gtctt 45

<210> 302  
<211> 709  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 302  
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60  
tccctcatgc tgccaccccc gactgtcact gcaccgaccg gccctcgagg acctgtctctt 120  
agggttcagaa gcgacccctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180  
cttcacctgg acgcccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240  
ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300  
gaagaccttc acttgactg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360  
ctcaaaatcc ggaacacat tccggcccga ggtccacctg ctgcccgcgc cgtcggagga 420  
gctggccctg aacgagctgg tgacgtgac gtgcctggca cgtggcttca gccccaagga 480  
tgtgctggtt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540  
ggcatcccgg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600  
cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattggtg gccacgaggc 660  
cctgccgctg gccttcacac agaagaccat cgaccgcttg gcgggtaaa 709

<210> 303  
<211> 236  
<212> PRT  
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 303

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Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
 20     25     30
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
 35     40     45
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
 50     55     60
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
 65     70     75
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
 85     90     95
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
100    105    110
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
115    120    125
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
130    135    140
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145    150    155
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
160    165    170
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
175    180    185
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
190    195    200
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
205    210    215
Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
225    230    235

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<210> 304

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 304

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gtcataattg ccagaggaca aattgtttct tcccagctct cagcaatcct gtctgcatct 120
ccagggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcct ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaacc ca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgtg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgttg 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctg cg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgaagtctgg 780
ggcagaggga ccacggtcac cgtctcttct gatcagccag tccctcaac tccacctacc 840
ccatctccct caactccacc taccctatct cctcatgct gccaccccg actgtcac tg 900
caccgaccgg ccctcgaggga cctgctctta gggttcagaag cgatcctcac gtgcacactg 960
accggcctga gagatgcctc aggtgtcacc ttccactgga cgccctcaag tgggaagagc 1020
gctgttcaag gaccacctga ccgtgacctc tgtggctgct acagcgtgtc cagtgtcttg 1080
ccgggctgtg ccgagccatg gaaccatggg aagaccttca cttgcactgc tgcctacc cc 1140
gagtccaaga ccccgctaac cgccacctc tcaaaatccg gaaacacatt ccggcccg ag 1200
gtccacctgc tgccgcccgc gtcggaggag ctggccctga acgagctggg gacgtga cg 1260
tgccctggcac gtggcttcag cccaaggat gtgctgtgtc gctggctgca ggggtcac ag 1320
gagctgcccc gcgagaagta cctgacttgg gcatcccggc aggagcccag ccagggca cc 1380

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
accaccttcg ctgtgaccag catactgcmc gtggcagccg aggactggaa gaagggggac 1440  
accttctcct gcatgggtgg ccacgagggc ctgccgctgg ccttcacaca gaagaccatc 1500  
gaccgcttgg cgggtaaa 1518

<210> 305  
<211> 502  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 305  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Pro Val Pro Ser  
260 265 270  
Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser  
275 280 285  
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu  
290 295 300  
Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg  
305 310 315 320  
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser  
325 330 335  
Ala Val Gln Gly Pro Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val  
340 345 350  
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr  
355 360 365  
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala  
370 375 380  
Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu  
385 390 395 400  
Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr  
405 410 415  
Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu  
420 425 430  
Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser  
435 440 445

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile  
450 455 460  
Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys  
465 470 475 480  
Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile  
485 490 495  
Asp Arg Leu Ala Gly Lys  
500

<210> 306  
<211> 924  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 306  
gcaacctaca tgatggggaa tgagttgacc ttcttagatg attccatctg cacggggcacc 60  
tccagtggaa atcaagtga cctcactatc caaggactga gggccatgga cacgggactc 120  
tacatctgca aggtggagct catgtaccca ccgccatact acctgggcat aggcaacgga 180  
accagattt atgtaattga tccagaaccg tgcccagatt ctgatcaacc caaatcttgt 240  
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc 300  
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 360  
tgctgtggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 420  
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 480  
cgtgtggtca gcgtctctac cgtctgcac caggactggc tgaatggcaa ggagtacaag 540  
tgcaagggtc ccaacaaagc cctcccagcc cccatcgaga aaacaatctc caaagccaaa 600  
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 660  
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 720  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 780  
gacggctcct tcttctctca cagcaagctc accgtggaca agagcagggtg gcagcagggg 840  
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 900  
ctctccctgt ctccgggtaa atga 924

<210> 307  
<211> 382  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 307  
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
1 5 10 15  
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
20 25 30  
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
35 40 45  
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
50 55 60  
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
65 70 75 80  
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95  
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110  
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr  
115 120 125  
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140  
Pro Cys Pro Asp Ser Asp Gln Pro Lys Ser Cys Asp Lys Thr His Thr  
145 150 155 160  
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe  
165 170 175  
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro  
180 185 190

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val  
 195 200 205  
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr  
 210 215 220  
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val  
 225 230 235 240  
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys  
 245 250 255  
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 260 265 270  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 275 280 285  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 290 295 300  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 305 310 315 320  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 325 330 335  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 340 345 350  
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 355 360 365  
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 370 375 380

<210> 308  
 <211> 453  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 308  
 atgggggtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60  
 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tgggtactggc cagcagccga 120  
 ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180  
 acagtgtctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240  
 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300  
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360  
 gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420  
 attgatccag aaccgtgccc agattctgat caa 453

<210> 309  
 <211> 151  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 309  
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
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 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro  
 20 25 30  
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
 35 40 45  
 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
 50 55 60  
 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
 65 70 75 80  
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
 85 90 95  
 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
 100 105 110  
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr  
 115 120 125

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140  
Pro Cys Pro Asp Ser Asp Gln  
145 150

<210> 310  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligo for engineering 14 amino acids from  
IgA-T4

<400> 310  
gttgtgatc agccagttcc ctcaactcca cctaccccat ctccctcaac t 51

<210> 311  
<211> 75  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 311  
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agcatggcga gcatg 75

<210> 312  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 312  
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala  
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Leu Leu Phe Pro Ser Met  
20

<210> 313  
<211> 372  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 313  
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gctgacagcc aggtgactga agtctgtgcg gcaacctaca tgacggggaa tgagttgacc 180  
ttcctagatg attccatctg cacgggcacc tccagtggaa atcaagtga cctcactatc 240  
caaggactga gggccatgga cacgggactc tacatctgca aggtggagct catgtacca 300  
ccgccatact acctgggcat aggc aaaggga accagattt atgtaattga tccagaaccg 360  
tgcccagatt ct 372

<210> 314  
<211> 124  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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 20      25      30
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
 35      40      45
Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr Phe Leu Asp Asp
 50      55      60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
 65      70      75      80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
 85      90      95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
100      105      110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
115      120
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```
<210> 315
<211> 1149
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> fusion polynucleotide
```

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<400> 315
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ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
acagtgcctc ggcaggctga cagccaggctg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
tggaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420
attgatccag aaccgtgccc agattctgat caaccctaat cttctgacaa aactcacaca 480
tccccaccgt ccccgaccac tgaactcctg gggggatcgt cagtcttctt cttcccccca 540
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 600
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 660
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 720
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cagcgggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1020
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tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1140
ggtaaatga                                     1149
```

```
<210> 316
<211> 382
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> fusion polypeptide
```

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<400> 316
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1      5      10      15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20      25      30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35      40      45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50      55      60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65      70      75      80
```

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<400>	317						
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ggcatcgcca	gctttgtgtg	tgagtatgca	tctccaggca	aagccactga	ggtccgggtg	180	
acagtgcttc	ggcaggctga	cagccagggt	actgaagtct	gtgcggcaac	ctacatgatg	240	
gggaatgagt	tgaccttctc	agatgattcc	atctgcacgg	gcacctccag	tggaaatcaa	300	
gtgaacctga	ctatccaagg	actgagggcc	atggacacga	gactctacat	ctgcaagggt	360	
gagctctatg	acccacgcgc	atactacctg	ggcataggca	acggaaccca	gatttatgta	420	
attgatccag	aaccgtgcc	agattctgat	cagccagttc	ccccaactcc	acctacccca	480	
tctccctcaa	ctccacctac	cccatctccc	tcagtctgcc	acccccgact	gtcactgcac	540	
cgacgggccc	tcgaggacct	gctcttaggt	tcagaagcga	tcctcactgt	cacactgacc	600	
ggcctgagag	atgctctcag	tgctcacctc	acctggacgc	cctcaagtgg	gaagagcgct	660	
gttcaaggac	cacctgaccg	tgacctctgt	ggctgctaca	gcgtgtccag	tgctctgcg	720	
ggctgtgccc	agccatggaa	ccatgggaag	accttcactt	gcactgctgc	ctaccccgag	780	
tccaagacc	cgctaaccgc	cacctctcca	aaatccggaa	acacattccg	gcccgaggtc	840	
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ctgccccgcg	agaagtacat	gacttgggca	tccgggcagg	agcccagcca	gggcaccacc	1020	
accttcgctg	tgactagcat	actgcgcgtg	cgacgcgagg	actggaagaa	gggggacacc	1080	
ttctctctga	tgggtggcca	cgaggccctg	ccgctgcgct	tcacacagaa	gaccatcgac	1140	
cgcttggcgg	gtaaaccac	ccatgtcaat	gtgtctgttg	tcatggcgga	ggttgacgac	1200	

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
acctgtctact gataatcttag a

1221

<210> 318  
<211> 403  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 318  
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20 25 30  
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu  
35 40 45  
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg  
50 55 60  
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met  
65 70 75 80  
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser  
85 90 95  
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp  
100 105 110  
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr  
115 120 125  
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu  
130 135 140  
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro  
145 150 155 160  
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg  
165 170 175  
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu  
180 185 190  
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val  
195 200 205  
Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro  
210 215 220  
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro  
225 230 235 240  
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala  
245 250 255  
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser  
260 265 270  
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu  
275 280 285  
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly  
290 295 300  
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu  
305 310 315 320  
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser  
325 330 335  
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala  
340 345 350  
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu  
355 360 365  
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly  
370 375 380  
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly  
385 390 395 400  
Thr Cys Tyr

<210> 319  
<211> 1209  
<212> DNA  
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 319

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ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggcccggtg 180
acagtgcctc ggcaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
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tctccctcaa ctccacctac cccatctccc tcatgctgcc accccgactg gtcactgcac 540
cgaccggccc tcgaggacct gctcttaggt tcagaagcga tcctcacgtg cacactgacc 600
ggcctgagag atgcctcagg tgtcaccttc acctggacgc cctcaagtgg gaagagcgtc 660
gttcaaggac cacctgaccg tgacctctgt ggctgctaca gcgtgtccag tgtcctgccg 720
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<210> 320

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 320

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Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35     40     45
Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50     55     60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65     70     75     80
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85     90     95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100    105    110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr
115    120    125
Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130    135    140
Pro Cys Pro Asp Ser Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro
145    150    155    160
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg
165    170    175
Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
180    185    190
Ala Ile Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val
195    200    205
Thr Phe Thr Trp Thr Pro Ser Gly Lys Ser Ala Val Gln Gly Pro
210    215    220
Pro Asp Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro
225    230    235    240
Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala
245    250    255
Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 260 265 270  
 Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu  
 275 280 285  
 Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly  
 290 295 300  
 Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu  
 305 310 315 320  
 Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser  
 325 330 335  
 Gln Gly Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala  
 340 345 350  
 Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu  
 355 360 365  
 Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly  
 370 375 380  
 Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp  
 385 390 395

<210> 321  
 <211> 328  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 321  
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 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180  
 cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240  
 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 300  
 atcgagaaaa ccatctccaa agccaaag 328

<210> 322  
 <211> 109  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 322  
 Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro  
 1 5 10 15  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 20 25 30  
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
 35 40 45  
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
 50 55 60  
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
 65 70 75 80  
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
 85 90 95  
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 100 105

<210> 323  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Amino acids surrounding the proline at 238

<400> 323

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
1 5 10

<210> 324  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Amino acid substitution of Serine for Proline at  
238

<400> 324  
Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser  
1 5 10

<210> 325  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligo to PCR IgE Fc

<400> 325  
gttggtgac acgtctgctc cagggacttc acccc 35

<210> 326  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' oligo to PCR IgE Fc

<400> 326  
gttggtttcta gattaacttt taccgggatt tacagacacc gctcgctgg 49

<210> 327  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligo to provide open reading frame at carboxy end  
of CH4 to read into transmembrane and cytoplasmic  
tail of another protein

<400> 327  
gttggttttcg aaggatccgc ttaccggga ttacagaca ccgctcgctg g 51

<210> 328  
<211> 996  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 328  
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cccagggact atcaacatca cctggctgga ggacgggcag gtcattggacg tggacttgtc 180  
caccgcctct accacgcagg agggtagct ggcctccaca caaagcgagc tcaccctcag 240  
ccagaagcac tggctgtcag accgcaccta cacctgccag gtcacctatc aaggtcacac 300  
ctttgaggac agcaccaaga agtgtgcaga ttccaacccg agaggggtga gcgcctacct 360  
aagccggccc agcccggttc acctgttcac ccgcaagtcg cccacgatca cctgtctggt 420

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 ggtggacctg gcacccagca aggggaccgt gaacctgacc tgggtcccggg ccagtgggaa 480  
 gcctgtgaac cactccacca gaaaggagga gaagcagcgc aatggcacgt taaccgtcac 540  
 gtccaccctg ccggtgggca cccgagactg gatcgagggg gagacctacc agtgcagggt 600  
 gaccaccccc cacctgcccc gggccctcat gcggtccacg accaagacca gcggcccgcg 660  
 tgctgccccg gaagtctatg cgtttgcgac gccggagtgg ccggggagcc gggacaagcg 720  
 caccctcgcc tgctgatcc agaacttcat gcctgaggac atctcgggtgc agtgggtgca 780  
 caacgaggtg cagctcccgg acgcccggca cagcacgacg cagccccgca agaccaaggg 840  
 ctccggcttc ttcgtcttca gccgcctgga ggtgaccagg gccgaatggg agcagaaaga 900  
 tgagttcatc tgccgtgcag tccatgaggc agcgagcccc tcacagaccg tccagcgagc 960  
 ggtgtctgta aatcccggta aagcggatcc ttcgaa 996

<210> 329  
 <211> 331  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 329  
 Asp His Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu  
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 Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu  
 20 25 30  
 Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp  
 35 40 45  
 Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr  
 50 55 60  
 Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser  
 65 70 75 80  
 Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr  
 85 90 95  
 Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp Ser Asn  
 100 105 110  
 Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro Phe Asp Leu  
 115 120 125  
 Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val Asp Leu Ala  
 130 135 140  
 Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala Ser Gly Lys  
 145 150 155 160  
 Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn Gly Thr  
 165 170 175  
 Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp Ile Glu  
 180 185 190  
 Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala  
 195 200 205  
 Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg Ala Ala Pro Glu  
 210 215 220  
 Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp Lys Arg  
 225 230 235 240  
 Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu Asp Ile Ser Val  
 245 250 255  
 Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His Ser Thr  
 260 265 270  
 Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Ser Arg  
 275 280 285  
 Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe Ile Cys  
 290 295 300  
 Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr Val Gln Arg Ala  
 305 310 315 320  
 Val Ser Val Asn Pro Gly Lys Ala Asp Pro Ser 330

<210> 330  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 330

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<210> 331

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 331

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<210> 332

<211> 91

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 332

gttggttgatc aggagcccaa atcttctgac aaaactcaca catctccacc gtccccagca 60  
cctgaactcc tgggtggacc gtcagtcttc c 91

<210> 333

<211> 1800

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 333

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ccaggggaga	aggtcacaat	gacttgcagg	gccagctcaa	gtgtaagtta	catgcactgg	180
taccagcaga	agccaggatc	ctcccccaaa	ccctggattt	atgccccatc	caacctggct	240
tctggagtcc	ctgctcgctt	cagtggcagt	gggtctggga	cctcttactc	tctcacaatc	300
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aatatgcact	gggtaaaagca	gacacctaga	cagggcctgg	aatggattgg	agctatttat	600
ccaggaaatg	gtgatacttc	ctacaatcag	aagttcaagg	gcaaggccac	actgactgta	660
gacaaatcct	ccagcacagc	ctacatgcag	ctcagcagcc	tgacatctga	agactctgcg	720
gtctatttct	gtgcaagagt	ggtgtactat	agtaactctt	actggtagct	cgatgtctgg	780
ggcacaggga	ccacggtcac	cgtctctgat	cacgtctgct	ccagggactt	caccccgccc	840
accgtgaaga	tcttacagtc	gtcctgcgac	ggcgggcgggc	acttcccccc	gacctccag	900
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tccacacaaa	gagagctcac	cctcagccag	aagcactggc	tgtagaccgc	cacctacacc	1080
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aaccgagag	gggtgagcgc	ctacctaagc	cggcccagcc	cggtcgacct	gttcatccgc	1200
aagtcgccc	cgatcacctg	tctggtggtg	gacctggcac	ccagcaaggc	gacctggaac	1260
ctgacctggt	cccgggccag	tggaagagcct	gtgaaccact	ccaccagaaa	ggaggagaag	1320
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gagggggaga	cctaccagtg	cagggtgacc	cacccccacc	tgcccagggc	cctcatgcgg	1440
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accagggccg	aatgggagca	gaaagatgag	ttcatctgccc	gtgcagtcca	tgaggcagcg	1740
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 334  
<211> 592  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

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20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Asp His Val Cys Ser Arg Asp  
260 265 270  
Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly  
275 280 285  
Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr  
290 295 300  
Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met  
305 310 315 320  
Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala  
325 330 335  
Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp  
340 345 350  
Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp  
355 360 365  
Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr  
370 375 380  
Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr  
385 390 395 400  
Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn  
405 410 415  
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg  
420 425 430  
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu  
435 440 445  
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg

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<400>	337						
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ggggagaaag	tcaccatcac	ctgccgtgcc	agctccagtg	taagttacat	gtactggtag	180	
cagcagaagt	caggcgcttc	ccttaaactc	tggatttatg	acacatccaa	gctggcttct	240	
ggagttccaa	atcggcttcag	tccagatggg	tctgggacct	cttattctct	cgcaattcaac	300	
accatggaga	ctgaagatgc	tgccacttat	tactgtcagc	agtggagtag	tacttcgctc	360	

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ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggaggga cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatca 785

<210> 338  
<211> 1491  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 338  
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ggggagaagg tcaccatcac ctgccgtgcc agctccagt taagttacat gtactgggtac 180  
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240  
ggagttccaa atcgcttcag tggcagtggg tctgggacct cttattctct cgcaatcaac 300  
accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360  
acgttcgggt ctgggaccaa gctggagatc aaacgggggtg gcggtggctc gggcgggtggt 420  
gggtcgggtg gcggcggatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgcaa 480  
ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatcaggagc ccaaactctg tgacaaaact cacacatgcc caccgtgcc agcacctgaa 840  
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgac 900  
tcccggagcc ctgaggtcac atgcgtggtg gtggacctga gccacgaaga cctgaggtc 960  
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020  
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080  
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctccagc ccccatcgag 1140  
aaaacaatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1200  
tcccgggatg agctgaccaa gaaccagggtc agcctgacct gcctggtcaa aggtctctat 1260  
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320  
acgcctcccg tgctggactc cgacggctcc ttcttctct acagcaagct caccgtggac 1380  
aagagcaggt ggacgcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440  
aaccactaca cgcagaagag cctctccctg tctccgggta aatgatctag a 1491

<210> 339  
<211> 1645  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> fusion polynucleotide

<400> 339  
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atgtccagag gagtgcacat tgtgtcact cagtctccaa caaccatagc tgcattctca 120  
ggggagaagg tcaccatcac ctgccgtgcc agctccagt taagttacat gtactgggtac 180  
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240  
ggagttccaa atcgcttcag tggcagtggg tctgggacct cttattctct cgcaatcaac 300  
accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360  
acgttcgggt ctgggaccaa gctggagatc aaacgggggtg gcggtggctc gggcgggtggt 420  
gggtcgggtg gcggcggatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgcaa 480  
ccgacacaga ccctgtccct cacatgcact gtctctgggt tctcattaac cagcgaatggt 540  
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600  
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacacc 660  
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720  
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatggtcac agtctcctct 780  
gatctggagc ccaaactctt tgacaaaact cacacaagcc caccgagccc agcacctgaa 840

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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ctcctggggg gatcgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgata 900
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aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1140
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1200
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtctctat 1260
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac 1380
aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcc tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aagcggatcc ttcgaaacctg 1500
ctcccatcct gggccattac cttaattctca gtaaatggaa tttttgtgat atgctgcctg 1560
acctactgct ttgcccgaag atgcagagag agaaggagga atgagagatt gagaagggaa 1620
agtgtacgcc ctgtataaat cgata 1645
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<210> 340  
<211> 1645  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

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ggggagaagg tcaccatcac ctgccgtgcc agctccagtg taagttacat gtactgggtac 180
cagcagaagt caggcgctc ccctaaactc tggatttatg acacatccaa gctggcttct 240
ggagttccaa atcgcttcag tggcagtggt tctgggacct ctattctctt cgcaatcaac 300
accatggaga ctgaagatgc tgccacttat tactgtcagc agtggagtag tactccgctc 360
acgttcgggt ctgggaccaa gctggagatc aaacgggggt gcggtggctc ggcggtgggt 420
gggtcgggtg gcggcgatc tcaggtgcag ctgaaggagg caggacctgg cctgggtgaa 480
cgcacacaga cctgtccct cacatgcact gtctctgggt tctcattaac cagcgatggt 540
gtacactgga ttcgacagcc tccaggaaag ggtctggaat ggatgggaat aatatattat 600
gatggaggca cagattataa ttcagcaatt aaatccagac tgagcatcag cagggaacac 660
tccaagagcc aagttttctt aaaaatcaac agtctgcaaa ctgatgacac agccatgtat 720
tactgtgcca gaatccactt tgattactgg ggccaaggag tcatgggtcac agtctcctct 780
gatctggagc ccaaactctt tgacaaaact cacacatgcc caccgtgccc agcacctgaa 840
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tcccggaccc ctgaggtcac atgctgtggt gtggacgtga gccacgaaga ccctgaggtc 960
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
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tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtctctat 1260
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
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aagagcaggt ggcagcaggg gaacgtcttc tcatgtctcc tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aagcggatcc ttcgaaacctg 1500
ctcccatcct gggccattac cttaattctca gtaaatggaa tttttgtgat atgctgcctg 1560
acctactgct ttgcccgaag atgcagagag agaaggagga atgagagatt gagaagggaa 1620
agtgtacgcc ctgtataaat cgata 1645
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<210> 341  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

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<400> 341
Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr Gln
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asp
20      25      30
Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met
35      40      45
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49076.000004pct2\_10.207.655 Seq List Text 07.24.03.txt  
Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile Lys  
50 55 60  
Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe Leu  
65 70 75 80  
Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala  
85 90 95  
Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser  
100 105 110  
Ser

<210> 342  
<211> 107  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 342  
Asp Ile Val Leu Thr Gln Ser Pro Thr Thr Ile Ala Ala Ser Pro Gly  
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Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met  
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Tyr Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp Ile Tyr  
35 40 45  
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Asn Arg Phe Ser Gly Ser  
50 55 60  
Gly Ser Gly Thr Ser Tyr Ser Leu Ala Ile Asn Thr Met Glu Thr Glu  
65 70 75 80  
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Thr Pro Leu Thr  
85 90 95  
Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 343  
<211> 258  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> fusion polypeptide

<400> 343  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
20 25 30  
Thr Ile Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
35 40 45  
Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
50 55 60  
Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
65 70 75 80  
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
85 90 95  
Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
115 120 125  
Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly  
130 135 140  
Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
145 150 155 160  
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
165 170 175  
Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser

<210> 344  
 <211> 492  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> fusion polypeptide

<400> 344  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15  
 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
 20 25 30  
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
 35 40 45  
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
 50 55 60  
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
 65 70 75 80  
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
 85 90 95  
 Ile Asn Thr Met Glu Thr Glu Asp Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly  
 130 135 140  
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
 145 150 155 160  
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
 165 170 175  
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 260 265 270  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 275 280 285  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 290 295 300  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 305 310 315 320  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 325 330 335  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 340 345 350  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 355 360 365  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 370 375 380  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 385 390 395 400  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 405 410 415  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 420 425 430  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 435 440 445  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 450 455 460  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 465 470 475 480  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 485 490

<210> 345  
 <211> 543  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 345  
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
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 Val Ile Met Ser Arg Gly Val Asp Ile Val Leu Thr Gln Ser Pro Thr  
 20 25 30  
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
 35 40 45  
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
 50 55 60  
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
 65 70 75 80  
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
 85 90 95  
 Ile Asn Thr Met Glu Thr Glu Asp Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly  
 130 135 140  
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
 145 150 155 160  
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
 165 170 175  
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 260 265 270  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 275 280 285  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 290 295 300  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 305 310 315 320  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 325 330 335  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
 340 345 350  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 355 360 365  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 370 375 380  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 385 390 395 400  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 405 410 415  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 420 425 430  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 435 440 445  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 450 455 460  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 465 470 475 480  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser  
 485 490 495  
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile  
 500 505 510  
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu  
 515 520 525  
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
 530 535 540

<210> 346  
 <211> 543  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 346  
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 20 25 30  
 Thr Ile Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Arg Ala  
 35 40 45  
 Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Ser Gly Ala  
 50 55 60  
 Ser Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
 65 70 75 80  
 Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Ala  
 85 90 95  
 Ile Asn Thr Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 Trp Ser Ser Thr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile  
 115 120 125  
 Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 Ser Gln Val Gln Leu Lys Glu Ala Gly Pro Gly Leu Val Gln Pro Thr  
 145 150 155 160  
 Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser  
 165 170 175  
 Asp Gly Val His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp  
 180 185 190  
 Met Gly Ile Ile Tyr Tyr Asp Gly Gly Thr Asp Tyr Asn Ser Ala Ile  
 195 200 205  
 Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Phe  
 210 215 220  
 Leu Lys Ile Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys  
 225 230 235 240  
 Ala Arg Ile His Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val  
 245 250 255  
 Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 275 280 285  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 290 295 300  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 305 310 315 320  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 325 330 335  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 340 345 350  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 355 360 365  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 370 375 380  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 385 390 395 400  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 405 410 415  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 420 425 430  
 Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser  
 435 440 445  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 450 455 460  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 465 470 475 480  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser  
 485 490 495  
 Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile  
 500 505 510  
 Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu  
 515 520 525  
 Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
 530 535 540

<210> 347  
 <211> 1527  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

<400> 347  
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 ggagacagag tcaccatcag ttgcagggca agtcaggaca ttcgcaatta tttaaactgg 180  
 tatcagcaga aaccagatgg aactgttaaa ctctgatct actacacatc aagattacac 240  
 tcaggagtcc catcaagggt cagtggcagt gggctctggaa cagattattc tctcaccatt 300  
 gccaacctgc aaccagaaga tattgccact tacttttgcc aacagggtaa tacgcttccg 360  
 tggacgttcg gtggaggcac caaactggta accaaacggg agctcggtg cgggtggctcg 420  
 ggcggtgggt ggtcgggtgg cggcggatct atcgtatgagg tccagctgca acagctgga 480  
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 ggctacatcg tgaactggct gaagcagagc catggaaaga accttgagt gattggactt 600  
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 actgtagaca agtcatccag cacagcctac atggagctcc tcagtctgac atctgaagac 720  
 tctgcagtct attactgtgc aagatctggg tactatgggt actcggactg gtacttcgat 780  
 gtctggggcg cagggaccac ggtcaccgtc tcctctgate aggagcccaa atcttgtgac 840  
 aaaactcaca catgcccacc gtgccagca cctgaactcc tggggggacc gtcagcttc 900  
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 960  
 gtgggtgggt acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1020  
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 gtggctcagc tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1140  
 aagggtctcca acaaagccct cccagcccc atcgagaaaa caatctccaa agccaaagg 1200  
 cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac 1260  
 caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg 1320  
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1380

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1440  
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1500  
tcctgtcttc cgggtaaatg atctaga 1527

<210> 348  
<211> 504  
<212> PRT  
<213> Artificial sequence

<220>  
<223> fusion polypeptide

<400> 348  
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1 5 10 15  
Val Ile Met Ser Arg Gly Val Asp Ile Gln Met Thr Gln Thr Thr Ser  
20 25 30  
Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala  
35 40 45  
Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp  
50 55 60  
Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly  
65 70 75 80  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu  
85 90 95  
Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln  
100 105 110  
Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Val  
115 120 125  
Thr Lys Arg Glu Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly  
130 135 140  
Gly Gly Gly Ser Ile Asp Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
145 150 155 160  
Leu Val Lys Pro Gly Ala Ser Met Ser Cys Lys Ala Ser Gly Tyr Ser  
165 170 175  
Phe Thr Gly Tyr Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn  
180 185 190  
Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr  
195 200 205  
Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
210 215 220  
Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala  
225 230 235 240  
Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr  
245 250 255  
Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Asp Gln  
260 265 270  
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
275 280 285  
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
290 295 300  
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
305 310 315 320  
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
325 330 335  
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
340 345 350  
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
355 360 365  
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
370 375 380  
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
385 390 395 400  
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
405 410 415  
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
420 425 430  
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
435 440 445

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 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 450 455 460  
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 465 470 475 480  
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 485 490 495  
 Ser Leu Ser Leu Ser Pro Gly Lys  
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<210> 349  
 <211> 2325  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fusion polynucleotide

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 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180  
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240  
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag tttaaccca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcggtggg 420  
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 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatattgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
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 tctccagcca ccctgtctgt gactccagga gactagagtct ctctttctcg cagggccagc 960  
 cagagtatta gcgactactt acactgggtat caacaaaaat cacatgagtc tccaaggctt 1020  
 ctcatcaaat atgcttccca ttccatctct gggatcccct ccagggttcag tggcagtggg 1080  
 tcagggtcag atttcactct cagtatcaac agtgtggaac ctgaagatgt tgggaatttat 1140  
 tactgtcaac atggtcacag ctttccgtgg acgttcggtg gaggcaccaa gctggaaatc 1200  
 aaacgggggt gcggtggctc gggcgagggt gggctcgggtg gcggcggtat tcagatccag 1260  
 ttggtgcaat ctggacctga gctgaagaag cctggagaga cagtcaggat ctctgcaag 1320  
 gcttctgggt atgccttcac aactactgga atgcagtggg tgcaagagat gccaggaaaag 1380  
 ggtttgaagt ggattggctg gataaacacc ccactctgga gtgccaaaat atgtagaaga 1440  
 cttcaaggac ggtttgctt ctctttggaa acctctgcca acactgcata ttacagata 1500  
 agcaacctca aagatgagga cacggctacg tatttctgtg tgagatccgg gaatggtaac 1560  
 tatgacctgg cctactttgc ttactggggc caagggacac tggctactgt ctctgatcag 1620  
 gagcccaaat cttctgacaa aactcacaca tccccaccgt cccagcacc tgaactcctg 1680  
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 ggcaaggagt acaagtcaa ggtctccaac aaagccctcc cagccccat cgagaaaaca 1980  
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 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 2100  
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgct 2160  
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 tacacgcaga agagcctctc cctgtctccg ggtaaatgat ctaga 2325

<210> 350  
 <211> 768  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> fusion polypeptide

<400> 350  
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

1 5 10 15  
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35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Ser Asn Ser Glu  
260 265 270  
Glu Ala Lys Lys Glu Glu Ala Lys Glu Glu Ala Lys Lys Ser Asn  
275 280 285  
Ser Val Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr  
290 295 300  
Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser  
305 310 315 320  
Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu  
325 330 335  
Leu Ile Lys Tyr Ala Ser His Ser Ile Ser Gly Ile Pro Ser Arg Phe  
340 345 350  
Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val  
355 360 365  
Glu Pro Glu Asp Val Gly Ile Tyr Tyr Cys Gln His Gly His Ser Phe  
370 375 380  
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly  
385 390 395 400  
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln Ile Gln  
405 410 415  
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Arg  
420 425 430  
Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Thr Thr Gly Met Gln  
435 440 445  
Trp Val Gln Glu Met Pro Gly Lys Gly Leu Lys Trp Ile Gly Trp Ile  
450 455 460  
Asn Thr Pro Leu Trp Ser Ala Lys Ile Cys Arg Arg Leu Gln Gly Arg  
465 470 475 480  
Phe Ala Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile  
485 490 495  
Ser Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg Ser  
500 505 510  
Gly Asn Gly Asn Tyr Asp Leu Ala Tyr Phe Ala Tyr Trp Gly Gln Gly  
515 520 525  
Thr Leu Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr  
530 535 540  
His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser  
545 550 555 560

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580 585 590  
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595 600 605  
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
610 615 620  
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
625 630 635 640  
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
645 650 655  
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
660 665 670  
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
675 680 685  
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
690 695 700  
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
705 710 715 720  
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
725 730 735  
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
740 745 750  
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
755 760 765

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<211> 1521  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 351  
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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
agcagagtgg aggtgaaaga tgctgccact tattactgcc agcagtgagg ttttaaccca 360  
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg 480  
aggcctgggg cctcagtga gatgtctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacagggg ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840  
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ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960  
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gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080  
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140  
tccaacaaag cctccccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200  
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc 1260  
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aatgggcagc cggagaacaa ctacaagacc acgctctccg tgctggactc cgacggctcc 1380  
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440  
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tctccgggta aatgatctag a 1521

<210> 352  
<211> 500  
<212> PRT  
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polypeptide

<400> 352

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 20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65      70      75
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 80      85      90
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 95      100      105
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 110      115      120
Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 125      130      135
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 140      145      150
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 155      160      165
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 170      175      180
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 185      190      195
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 200      205      210
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 215      220      225
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 230      235      240
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 245      250      255
Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu
 260      265      270
Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 275      280      285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 290      295      300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 305      310      315
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 320      325      330
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 335      340      345
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 350      355      360
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 365      370      375
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 380      385      390
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 395      400      405
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 410      415      420
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 425      430      435
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 440      445      450
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 455      460      465
Ser Pro Gly Lys
 470      475      480
500
 485      490      495

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<210> 353  
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<220>  
<223> fusion polynucleotide

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tgcacagtct ctggtttctc attaaactacc tatgctgtac actgggttcg ccagtcctca 180  
ggaaagggtc tggagtggtt gggagtgata tggagtggtg gaatcacaga ctataatgca 240  
gctttcatat ccagactgag catcaccaag gacgattcca agagccaagt tttctttaaa 300  
atgaacagtc tgcaacctaa tgacacagcc atttattact gtgccagaaa tgggggtgat 360  
aactaccctt attactatgc tatggactac tggggctcaag gaacctcagt caccgtctcc 420  
tca 423

<210> 354  
<211> 366  
<212> DNA  
<213> qArtificial Sequence

<220>  
<223> fusion polynucleotide

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ccaggaaagg gtctggagtg gctgggagtg atatggagtg gtggaatcac agactataat 180  
gcagctttca tatccagact gagcatcacc aaggacgatt ccaagagcca agttttcttt 240  
aaaatgaaca gtctgcaacc taatgacaca gccatttatt actgtgccag aaatgggggt 300  
gataactacc cttattacta tgctatggac tactgggggtc aaggaaacctc agtcaccgtc 360  
tcctca 366

<210> 355  
<211> 399  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 355  
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gatattgtga tgacgcaggc tgcattctcc aatccagtc cttctggaac atcagcttcc 120  
atctcctgca ggtctagtaa gagtctccta catagtaatg gcatcactta tttgtattgg 180  
tatctgcaga agccaggcca gtctcctcag ctccgtgatt atcagatgtc caaccttgcc 240  
tcaggagtc cagacagggt cagtagcagt gggtcaggaa ctgatttcac actgagaatc 300  
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ctcacgttcg gtgctgggac caagctggag ctgaaacgg 399

<210> 356  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fusion polynucleotide

<400> 356  
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acatcagctt ccatctcctg caggctcagt aagagtctcc tacatagtaa tggcatcact 180  
tatttgattt ggtatctgca gaagccaggc cagctctctc agctcctgat ttatcagatg 240  
tccaaccttg cctcaggagt cccagacagg ttcagtagca gtgggtcagg aactgatttc 300  
acactgagaa tcagcagagt ggaggctgag gatgtgggtg tttattactg tgctcaaaat 360  
ctagaacttc cgctcacgtt cggtgctggg accaagctgg agctgaaacg ggggtggcgtt 420